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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                 August 29, 2001, 15:04:42; Search time 1774.1 Seconds (without alignments) 130.780 Million cell updates/sec
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                 tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                          1344157 seqs, 7733874588 residues
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Maximum Match 100%
Listing first 45 summaries
                                                           OM nucleic - nucleic search, using sw model
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Searched:

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Title:

A70378 Sequence 8 AX095547 Sequence M94144 Mus musculu M64874 Mouse inter D88111 Homo sapien AF115754 Equus cab G65440 stdJ388M5\_1 AF043127 Homo sapi

A/05.6 AX095547 MUSAIC2A09 MUSIL4R07 D88111 ECIL/7R1 G65440 8 HSIL/7R5

A70378 ΩI

Description

SUMMARIES

30-MAR-2001

PAT

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Mus musculus
Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Gorman,D.M., Itoh,N., Jenkins,N.A., Gilbert,D.A., Copeland,N.G. and
Miyajima,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chromosomal localization and organization of the murine genes encoding the beta subunits (AIC2A and AIC2B) of the interleukin 3, granulocyte/macrophage colony-stimulating factor, and interleukin
                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 21)
Lander, E.S., Gargill, M., Ireland, J.S., Bolk, S., Daley, G.Q. and Mccarthy, J.J.
Single nucleotide polymorphisms in genes
Patent: WO 0118250-A 725 15-MAR-2001;
WHITEBEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium
                                                                                                                                                                                                                                                                                                                                                                                                                            MUSAIC2A09 160 bp DNA ROD 27-APR-19 WLMS musculus IL-3 receptor B-subunit (AIC2A) gene, exon 10. M94144 GI:191815
                                                                                                                                                                                                                                                                                                            92.0%; Score 13.8; DB 10;
86.7%; Pred. No. 7.2e+02;
iive 2; Mismatches 0;
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92348451
                                                      AX095547 21 bp DNA
Sequence 725 from Patent W00118250.
AX095547
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/db_xref="taxon:9606"
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AC072998 Giardia i
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AF029294 Mustela v
AF169792 Ursus mar
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X6178 Human HSIL5
A70386 Sequence 16
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D88110 Homo sapien
I19684 Sequence 6
E09304 Human CDNA
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AR031384 Sequence
AL414415 T3 end of '
119683 Sequence 5
E09303 Human cDNA
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I19685 Sequence 8
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  I21102 Sequence 73
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AC041965 Giardia i
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114817 Sequence 11
U04361 Canis famil
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AR040674 Sequence
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                                                                           AR031381 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 15)
Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
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100.0%; Pred. No. 7.1e+02;
ive 0; Mismatches 0;
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/organism="unidentified"
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a 7 c 0 g 3
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121102
HUMIL2RG05
CNS01DQR
AC072998
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AR031381
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E09305
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CNS072TH
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A70378.1 GI:4774659
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Nishikawa, N.
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Wrighton, N., Campbell, L.A., Harada, N., Miyajima, A. and Lee, F. The murine interleukin-4 receptor gene: genomic structure, expression and potential for alternative splicing Growth Factors 6 (2), 103-118 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (strain:HeLa) DNA, clone_lib:libraly of clones containing poly(dG)poly(dC)library clone:pHGC40L.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="'approx. 1.4kb 3' of segment 6'; 'interleukin-4
receptor'; putative"
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Pred. No. 8e+02;
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<1. .25
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    /organism="Mus musculus"

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/note="putative"
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            Best Local Similarity 80.0
Matches 12; Conservative
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Caetano, A.R., Lyons, L.A., Laughlin, T.F., O'Brien, S.J., Murray, J.D. and Bowling, A.T.
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1 (bases 1 to 248)
Caetano, A.R., Lyons, L.A., Laughlin, T.F., O'Brien, S.J., Murray, J.D. and Bowling, A.T.
Equine synteny mapping of comparative anchor tagged sequences (CATS) from human Chromosome 5
Mamm. Genome 10 (11), 1082-1084 (1999)
                                                                                                                                                                                                                                                         3 (sites)
Nishikawa,N., Kanda,N., Oishi,M. and Kiyama,R.
Nishikawa,N., Kanda,N., Oishi,M. and Kiyama,R.
Shrichment of Oligo(dG).Oligo(dC)-containing fragments from human genomic DNA by Mg 2+-dependent triplex affinity capture
Nucleic Acids Res. 25 (9), 1701-1708 (1997)
                                    Naoko
Submitted (28-SEP-1996) to the DDBJ/EMBL/GenBank databases. Naok Submitted (28-SEP-1996) to the DDBJ/EMBL/GenBank databases. Naok Nishikawa, Univ. Tokyo, Ins. Mol. Cell. Biosci.; Yayoi 1-1-1, Bunkyo-ku, Tokyo 113, Japan (Tel:03-3812-2111(ex.7877), Fax:03-3818-9437)

Z. (bases 1 to 213)

Nishikawa, N., Oishi, M. and Kiyama, R.

Enrichment of poly(d6), poly(dC)-containing fragments from human genomic DNA by Mg2+-dependent triplex affinity capture
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Equus caballus interleukin-7 receptor (IL/R) gene, partial
sequence.
AF115754
AF115754 I GI:6469582
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/clone="mpfc30b;
/clone_lib="libraly of clones containig
poly(dG)poly(dC)library"
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/strain="HeLa"
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Puel, A., Zlegler, S.F., Buckley, R.H. and Leonard, W.J.
Direct Submission
Submitted (15-JAN-1998) Immunology, Virginia Mason Research Center, 1000 Seneca St., Seattle, WA 98101, USA
Location/Qualifiers
                                                                                                                                                                                                                                               Homo sapiens
Bukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 403)
Puel.A., Zitegler,S.F., Buckley,R.H. and Leonard,W.J.
Defective IL/R expression in T(·)B(+)NK(+) severe combined
immunodeficiency
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Homo sapiens interleukin-7 receptor precursor (IL7R) gene, exon
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Leonard,W.J., Noguchi,M. and McBride,O.Wesley.
Methods for diagnosis of XSCID and Kits thereof
Patent: US 5518880-A 73 21-MAY-1996;
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/number=5
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    12; Conservative
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265 ACTCCATTCACTCCA 251
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Primer A: GAAGTGCAGAGGGAAACTGC
Primer B: GACTCAGACCAGGTCCTGGA
STS size: 367
PCR Profile:
                                                                                                                                                                                                                                                                                                                              Dawson, E., Chen, Y., Hunt, S. and Dunham, I.
Extraction and analysis of SNP data from genomic sequence of human chromosome 22
                                                                                                                                                                                                                                                                                          Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 367)
                                                                                                                                                                     $65440 367 bp DNA STS 19-JUL-2000 std3388MS_151462 chromosome 22 genomic clone Homo sapiens STS genomic clone 388MS, sequence tagged site.
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   Score 13.8; DB 7; Length 248;
Pred. No. 8e+02;
3; Mismatches 0; Indels
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/db_xref="taxon:9606"
/clone="388M5"
/clone=lib="chromosome 22 genomic clone"
1. 367
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2-mercaptoethanol: 10mM
Taq Polymerase: 0.04 units/ul
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67 mM fris-HCl
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pH: 8.8
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Synonyms: stSG73865
Contact: Ian Dunham
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                          1 (bases 1 to 490)
Noguchi,M., Adelstein,S., Cao,X. and Leonard,W.J.
Characterization of the human interleukin-2 receptor gamma chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78025 Versailles, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
   Gaps
                                                                                                                              HUMIL2RG05 490 bp DNA PRI 06-JAN-1995
Human interleukin 2 receptor gamma chain (IL2RG) gene, exon 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA 03-SEP-1999
T4 cDNA library under conditions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungl; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Sclerotiniaceae; Botryotinia.

1. (bases I to 537)

Bitton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y. Direct Submission
                                                                                                                                                                                                                   Homo sapiens (tissue library: Charon 4A) fetus liver DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
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   Indels
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93293887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.8; DB 97;
Pred. No. 8.3e+02;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                order(L12179.1:221. .423,1. .125)
 ;
0
   Mismatches
                                                                                                                                                           L12180.1 GI:307053
interleukin 2 receptor gamma chain.
5 of 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA library; nitrogen deprivation.
Botryotinia fuckeliana.
Botryotinia fuckeliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="liver"
/tissue_lib="Charon 4A"
                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Botrytis cinerea strain
nitrogen deprivation.
AL117163
AL117163.1 GI:5832379
 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /number=4
126. .288
/gene="IL2RG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.0%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /number=5
127 c
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 Conservative
                                                         254 GCTCCATTCACTCCA 240
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254 GCTCCATTCACTCCA 240
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                            RCTCCAYTCRCTCCA 15
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                                                                                                                                                                                                                                     Homo sapiens
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12;
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                                                                                                   RESULT 10
HUMIL2RG05/c
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DEFINITION
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CNS01DQR/c
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JOURNAL
 Matches
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AUTHORS
TITLE
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Nixon,J., Morrison,H.G., McArthur,A.G., Eakin,N.O., Kim,U., Crocker,M.C., Hinkle,G., Holder,M.E. and Sogin,M.L. Direct Submission

Direct Submission

Submitted (07-JUN-2000) Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA

* NOTE: This record contains 1 individual into sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.

* However, it should not be assumed this clone will be sequenced to completion. In the event that the record is updated, the accession number will
CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII vector.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC072998 572 bp DNA HTG 07-JUN-2000
Giardia intestinalis clone NJ4660 strain WB-C6, LOW-PASS SEQUENCE
SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia. 1 (bases 1 to 572)
Morrison, H.G., McArthur, A.G., Nixon, J., Eakin, N.Q., Kim, U., Crocker, M.C., Hinkle, G., Holder, M.E. and Sogin, M.L. Giardia: a model for ancient eukaryotic genome analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 537;
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                                                                                                                                                                                                                                                                       1. .537
/organism="Botryotinia fuckeliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 13.8; DB 14;
Pred. No. 8.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Giardia intestinalis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        /note="Genoscope sequence
46 c 178 g 176
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                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:40559"
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                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:8325346
                                                                                                                                                                                                                                                                                                                           /strain="T4"
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80.0%;
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Giardia intestinalis
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/translation="KPGEDGGLPTKYTLTYHKEGETTTHECPDYITSGPNSCYFNKKH
TSIWTMYITTINATNEMGSSSSDPRYVTLTYIVEPDPPVNLSLELKQPEDKKTYLMIK
WYPPTLVDVRSGWLTLQYEIRKKPEKATEWETHFAGLOTOFKILSLYEGGKYLVQVRC
KPDHGFWASEWSFRSTQIPNDISMKDTIVWIFVAVLSAVICLIMVAAVALKGHSMYT"
159 c 1159 c 1153 t
                        Douglas,D.A., Houde,A., Song,J.H., Farookhi,R., Concannon,P.W. and
Murphy,B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Buteleostomi; Carnivora; Fissipedia; Ursidae; Ursus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (19-JUL-1999) Curriculum in Toxicology, University of North Carolina, MD-72, US EPA, Research Triangle Park, NC 27711,
                                                                Lutering the normone receptors in the ovary of the mink (Mustela vison) during delayed implantation and early-postimplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cloning, sequence analysis, and seasonal mRNA expression of the extracellular region of the lutebilizing hormone receptor (LHF), follicle-stimulating hormone receptor (FSHF), and prolactin receptor (PRLF) genes in the testis of the black bear (Ursus
                                                                                                                                                                                          Conses 1 to 652)

Douglas,D.A., Song,J.-H., Houde,A. and Murphy,B.D.

Douglas,D.A., Song,J.-H., Houde,A. and Murphy,B.D.

Direct Submission

Submitted (08-007-1997) Agriculture and Agri-Food Canada, Food Research and Development Centre, 3600 Casavant Blvd. West, St-Hyacinthe, Quebec J2S BE3, Canada

Location/Qualifiers

1. 652

/organism="Mustela vison"

/db_xref="taxon:9667"

/Lissue_type="testis"

1. .552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Ursus maritimus prolactin receptor mRNA, partial cds.
AF169792
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Pred. No. 8.4e+02;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="prolactin receptor"
                                                                                                                            Biol. Reprod. 59 (3), 571-578 (1998)
98384190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AABBBBB99.1"
/db_xref="GI:2688975"
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Howell-Skalla, L.A. and Bahr, J.M.
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1. .681
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80.0%;
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Mammalia; Eutheria;
1 (bases 1 to 681)
        1 (bases 1 to 652)
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514 GCTCCACTCACTCCA 500
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Eakin, N. O., Morrison, H.G., McArthur, A.G., Nixon, J., Kim, U., Crocker, M.C., Hinkle, G., Holder, M.E. and Sogin, M.L.

Crocker, M.C., Hinkle, G., Holder, M.E. and Sogin, M.L.

Direct Submission

Submitted (02-APR-2000) Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, 7

MBL Street, Woods Hole, MA 02543-1015, USA

* NOTE: This record contains 1 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence Sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will
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Mammalia, Eutheria, Carnivora, Fissipedia, Mustelidae, Mustela.
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Mustela vison prolactin receptor (PRLr) mRNA, partial cds.
AF029294
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia. 1 (bases 1 to 585) Morison, H.G., McArthur, A.G., Nixon, J., Eakin, N.Q., Kim, U., Crocker, M.C., Hinkle, G., Holder, M.E. and Sogin, M.L. Glardia: a model for ancient eukaryotic genome analysis Unpublished
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      Pred. No. 8.3e+02;
3; Mismatches 0;
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Pred. No. 8.3e+02;
3; Mismatches 0;
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HTG; HTGS_PHASE0.
Glardia intestinalis.
Glardia intestinalis
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80.0%;
    80.08;
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Matches 12; Conservative
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Best Local Similarity 80.0
Matches 12; Conservative
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Ash...c.
3JT, UK.
Tel: +44 131 650 6760
Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk
The Ascaris suum EST dataset (including the ASC clustering
information) is available on the www at http://www.ed.ac.uk/(tilde.)
inbx/AscarisWeb/AscarisEST.html
PCR PRimers
FORMARD: M13 Reverse (AGCGGATAACAATTTCACACAGGA)
BACKWARD: M13 Reverse (AGCGGATAACAATTTCACACAGGA).
Seq primer: M13 Reverse (AGCGGATAACAATTTCACACAGGA).

Location/Qualifiers

135
                                                                                                                                                                                                       Bukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea; Ascarididae; Ascaris:
1 (bases I to 315)
1 (bases I to 315)
1 Daub, J., Geary, T. and Blaxter, M.
A survey of genes expressed in the parasitic nematode Ascaris suum Contact: Blaxter M.
Contact: Blaxter M.
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW165758 315 bp mRNA EST 12-NOV-1999 MBASBWA080M13R Ascaris suum (parasitic nematode) body wall muscle and hypodermis Ascaris suum cDNA clone MBASBWA080 5', mRNA
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/organism="Ascaris suum" .

/db_ref="*exon.6253"

/clone="MBASBWA080"

/clone="Lib="Ascaris suum (parasitic nematode) body wall

/sex="mixed"
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                                                                                 sequence.
AW165758
AW165758.1 GI:6382633
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Best Local Similarity 80.0
Matches 12; Conservative
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Ascaris suum
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1 RCTCCAYTCRCTCCA 15
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Rodentla; Sclurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 302)

1 Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,

1 Ehli, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai,

C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,

Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,

Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata,

Y., Shigemoto, Y., Shiraki, T., Soquebe, Y., Sugahara, K., Shibata,

Y., Shigemoto, Y., Shiraki, T., Soquebe, Y., Sugahara, Y., Suzuki, H.,

Matahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T.,

Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T.,

Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T.,

Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T.,

Ontact: Yoshihide Hayashizaki

Genome Exploration Research Group, Life Science Tsukuba Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Automated filtration based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                            ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genome-res@rtc.riken.go.jp,
WLihttp://genome-rtc.riken.go.jp,
Saski,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
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The Institute of Physical and Chemical Research (RIKEN), Genomic
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/clone_lbb="RIKEN full-length enriched, 8 days embryo"
/sex="mixed" 8 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                              AV298115 302 bp mRNA EST 10-NOV-1999 AV298115 RIKEN full-length enriched, 8 days embryo Mus musculus
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                                                                                                                                                                            Gaps
5' end: SalI; 3' end: BamHI."
102 t
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                                                                                                                         Score 13.8; DB 123; Length 299; Pred. No. 2.8e+03;
                                                                                                                                                                         0; Indels
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                 , mRNA sequence.
                                                                                                                                                                         3; Mismatches
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AV298115
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Zabarovsky, P.R., Glatullin, R., Podowski, R.M., Zabarovska, V.V., Xie
L., Muravenko, O.V., Kozyrev, S., Petrenko, L., Skobeleva, N., Li, J.,
Protopopov, A., Kashuba, V., Ernberg, I., Winberg, G. and Wahlestedt, C.
NotI clones in the analysis of the human genome
Nucleic Acids Res: 28 (7), 1635-1639 (2000)
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                                                                                   RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5" GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTVN 3'], cDNA was
/note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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NB6-223C Human NotI clones Homo sapiens genomic, DNA sequence.
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Pred. No. 2.8e+03;
3; Mismatches 0;
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/db_xref="taxon:9606"
/clone_lib="Human NotI clones"
148 c 74 q 43 t.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center for Genomics Research
Karolinska Institute
1717 Stockholm, Sweden
Tel: +46-8-728-6372
Fax: +46-8-337983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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AQ937634.1 GI:7214012
                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Podowski
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E (Annuality Description (Countries) Scillogianis; musicae; musica
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URL:http://genome.rtc.riken.go.jp,
Carninci.p., Nishiyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
Carninci.p., Nishiyama.Y., Mestover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,
Y. and Hayashizaki,Y.
                                                                                                                                 Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Science Laboratory The Institute of Physical and Chemical Research (RIKEN), Genomic
                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninoi, P. and Hayashizaki, Y.
High-efficiency full-length CDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
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/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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/clone="5330424007"
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                                                              Mus musculus
Eukaryota; Metazoa;
                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sciences Center
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                                                              ORGANISM
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JOURNAL
                                                                                                                                                           REFERENCE
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KEYWORDS
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                                 SOURCE
                                                                                                                                                                            Email: genome-resertc.riken.go.jp,
URL: http://genome.rtc.riken.go.jp,
URL: http://genome.rtc.riken.go.jp,
Carninci,P. Nishiyama,Y. Westover,A. Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB024897 RIKEN full-length enriched, adult male pituitary gland Mus musculus cDNA clone 5330424007 3', mRNA sequence.
BB024897.1 GI:8198974
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                          The Institute of Physical and Chemical Research (RIKEN), Genomic
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Pred. No. 2.8e+03;
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                                                                                            Tsukuba, Ibaraki 305-0074, Japan
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/dev_stage="13 days embryo"
/lab_host="DH10B"
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/clone="5930436B16"
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   Genome Science Laboratory
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80.0%;
                                                                                                                       Tel: +81-298-36-9013
Fax: +81-298-36-9098
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Best Local Similarity 80.0
Matches 12; Conservative
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                                                           Sciences Center
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FEATURES

RESULT 12

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BB024897

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AF061117 Rice Millyang 117 suspension culture mRNA Oryza sativa AF061117
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                                                                                             AF061117.1 GI:3114679
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                                                                                                                                                                                                                                        AUTHORS
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URL:http://genome-resertc.riken.go.jp,
Carninci.P. Nishiyama.Y. Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayshizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
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CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Y. and Hayashizaki,Y. Ozama,Y., Ozawa,Y., Muramatsu,M., Okazaki
Automated filtration-based high-throughput plasmid preparation
System. Genome Res. 9 (5), 463-470 (1999)
Garninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Watanatsu,M. and Hayashizaki,Y.
TKIKEN Mouse ESTS (Konno,H., et al.)
Unpublished (2000)
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                                                                                          Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
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/organism="Mus musculus"
/organism="Mus musculus"
/organism="657BL/63"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="5390420L02"
/clone="1ib="RIKEN full-length enriched, adult male pituitary gland"
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Pred. No. 2.8e+03;
3; Mismatches 0; Indels 0;
                                                                                                                                                                            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
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Matches 12; Conservative
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FEATURES

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Judge musculus Schordata; Craniata; Vertebrata; Euteleostoml; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Eukaryota; Metazoa; Chordata; Craniata; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 297)

Ronno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fitudao, S., Fikunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, T., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matayama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shipaa, K., Shipamoto, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Yokota, T., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yokota, T., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yamamura, T., Yanusatsu, M. and Hayashizaki, Y., Mullished (2000)

Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                          1 (bases 1 to 297)

Kim,C.Y., Cheon,S.Y. and Cho,M.J.

Isolation and Characterization of Fungal Elicitor Responsive Rice
Genes by mRNA Differential Display
Unpublished (1998)

Contact: Kim, Cha Young
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4530"
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/clone_lib="Rice Millyang 117 suspension culture mRNA"
/note="suspension culture"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                      900 Gajwa-dong, Chinju, Kyeong-nam 660-701, Korea
Email: choslab@nongae.gsnu.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 13.8; DB 14;
Pred. No. 2.8e+03;
3; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa"/cultivar="Millyang 117"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
COMMENT
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SM Mus musculus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Musmania; Euteleostomi; Musmania; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 295)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishiikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, T., Kal, C., Kawai, J., Ishikawa, T., Itoh, M., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saitoh, H., Saitoh, H., Saitoh, H., Saitoh, H., Shiharak, A., Shibata, Y., Shigamoto, Y., Shinaqawa, A., Shiharaki, T., Soqabe, Y., Suqahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB024272 23-JUN-2000 BB024272 RIKEN full-length enriched, adult male pituitary gland Musmusculus cDNA clone 5330420L02 3', mRNA sequence.
                        Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 287)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Worris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Morris,M., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                       Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton University Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.0%; Score 13.8; DB 9; Length 287; 80.0%; Pred. No. 2.7e+03; ive 3; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="IMAGE:972918"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vector to vector length is 288
Seq primer: -28ml3 revl ET from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                       Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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160 ACTCCACTCGCTCCA 146
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        Mus musculus
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                                                                                                                                                                                 Waterston, R.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
and minmatch 12 options.
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Fabrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E. Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
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IMAGE:972918 5' similar to gb:M29697 Mouse interleukin-7 receptor
(MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
                             Gaps
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                                                                                                                                                                                                                   AW417497 275 bp mRNA EST
4258 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
AW417497.1 GI:6945379
                          Indels
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    Pred. No. 2.7e+03;
3; Mismatches 0;
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/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="WARC IPIG"
/tissue_type="pooled"
/lab_host="DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORWARD: AGGAAACAGCTATGACGAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 20 row. K column: 3
Seq prime: ATTTAGGTGACACTATAG.
Location/Qualifiers
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    80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Smith TPL
Best Local Similarity 80.0
Matches 12; Conservative
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16 ACTCCATTCACTCCA 30
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Matches 12; Conserv
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Sus scrofa
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AUTHORS
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Konno, H., Atzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itch, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M. Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, Y., Shigemoto, Y., Shinayawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Yokota, T., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, M., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-resertc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
Carninci.p., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
Carninci.p., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGAGAGAGAGGATCCAAGACTCTTTTTTTTTTTTTTVN 3'), cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="wolffian duct includes surrounding region"
/dev_stage="12 days embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTATTAATTAATCCCCCCCCCCC 3'). cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y. and Hayashizaki,Y. Julbaca,I., Uzawa,Y., Muramatsu,M., Okaz, Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carinoi,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RIKEN full-length enriched, 12 days embryo male wolffian duct"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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/clone="6720436D12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sciences Center
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ORIGIN
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JOURNAL
     REFERENCE
                            AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 256)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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                                                                                                                                                                                                                                                 AQ548570 256 bp DNA GSS 28-MAY-1999
CITBI-E1-2635F16.TF CITBI-E1 Homo sapiens genomic clone 2635F16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
     Indels
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     Mismatches
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/clone="2635F16"
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/note="Vector: pBel
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m
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80.0%;
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     Conservative
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175 GCTCCACTCACTCCA 161
                                                                                   :|||||:||:|||||
107 ACTCCACTCGCTCCA 121
                                                      RCTCCAYTCRCTCCA 15
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                                                                                                                                                                                                                                                                                                                DNA sequence.
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AQ548570/c
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Gaps

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Length 201;

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/note-"Organ: breast, Vector: puc18; Site_1: Smal; Site_2: Smal; A min-11brary was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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1 (bases 1 to 248)

Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
Waterston, R. and Wilson, R.,
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AISO5954 248 bp mRNA EST 11-MAR-1999 vl21f12.xl Stratagene mouse Tcell 937311 Mus musculus CDNA clone IMAGE:972911 3' similar to gb:M29697 Mouse interleukin-7 receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                               Score 13.8; DB 163; Length
Pred. No. 2.7e+03;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M/WashU-NCI Mouse EST Project 1999
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    /dev_stage="Adult"
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Best Local Similarity 80.0.
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Fax: 314 286 1810
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43 GCTCCACTCACTCCA 29
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I (bases 1 to 201)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2-MR2-BT0590-100
300-118-c08_lts1=20000-031-0&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 201.
Location/Qualifiers
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v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                           /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
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Pred. No. 2.6e+03;
3; Mismatches 0; I
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/db_xref="taxon:9606"
/clone_lib="BT0590"
                                                                                                                                                                                     1. .173
/organism="Bos taurus"
                                                                                                                                                                                                                                 /db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
                                                                 FORMARD: AGGAAACAGCTATGACCAT
BACKNARD: GTTTTCCAGTACAGGACG
Plate: 40 row: J column: 24
Seg primer: ATTTAGGGTGACACTATAG.
                                                                                                                                                                                                                                                                               /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                Location/Qualifiers
                     and -minmatch 12 options. PCR PRimers
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BE076128.1 GI:8425639
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RESULT

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ORIGIN

TITLE

COMMENT

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Score 13.8; DB 21; Length 248; Pred. No. 2.7e+03;
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:972911"
/clone_lib="Stratagene mouse Tcell 937311"
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Result No.

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MEDLINE 97044477  COMMENT Contact: Chin, H  National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9443, USAA	Tel: 301 443 1700 Fax: 301 443 9890 Email: mEST@mail.nih.gov Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. CDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BWAP CDNAS whose availability will be considered under appropriate and limited collaborative arrangements of primer: M13 Forward	FEATURES Location/Qualifiers  1. 151 Source Location/Qualifiers 1. 151 Source Location="C57BL/G1" Strain="C57BL/G1" Strain="C5BL/G1" Strain="C5BL/	NIH_BWAP_MHIZ_SI_library is a subtracted library derived from NIH_BWAP_MHIZ. NIH_BWAP_MHIZ is a library derived from mouse hippocampus tissue. For a detailed description of the library from which this clone was 'derived, please visit our web site at brainest.eng.ulowa.edu.  TAG_SEQ-None found"  BASE COUNT  31 a 34 c 48 g 38 t  ORIGIN	Ouery Match 92.0%; Score 13.8; DB 149; Length 151; Best Local Similarity 80.0%; Pred. No. 2.6e+03; Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0; Qy 1 RCTCCAYTCRCTCA 15 :	RESULT 2 BF601415/c LOCUS BF601415 173 bp mRNA EST 13-DEC-2000 LOCUS DEFINITION 266391 MARC 3BOV BOS taurus CDNA 5', mRNA sequence. ACCESSION BF601415.1 GI:11698637 VERSTON BF601415.1 GI:11698637 KEYWORDS EST. SOURCE COW. ORGANISM BOS taurus ORGANISM BOS taurus Dikarvora: Matazoa: Chordata: Craniata: Vertebrata: Euteleostomi:	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea; Bovidae; Bovidae; Bovidae; Bos.  Reference (base) 1 to 173)  AUTHORS Smith, T.P. L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Laegreid, W.W., and Keele, J.W.  TITLE Design and use of four pooled tissue normalized cDNA libraries for besign and use of four pooled tissue normalized cDNA libraries for Unpublished (2000)  COMMENT Contact: Smith TPL  USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4396 Fax: 402 762 4396
SUMMARIES Description	149 BF488328 151 BF601415 163 BE076128 21 AISOS954 230 AQ548570 124 BB05188 115 BB05188 BB05188 115 BB05188 BB05188 115 BB05188 BB05188 115 BB05477 14 AF061117 15 BB02427	124 BB024897 BB024897 28 AV298115 AV298114 AV2972 ZEV244 AV25404 AV251043 AV21043 AV21043 AV21043 AV272 ZEV2404 AV251043 AV21043	30 AV406268 A 136 BE517357 BE517357 9 AA621706 A621706 at 230 AO545960 AO545960 150 BF524586 AW074425 222 AW074425 AW074425 115 AW406187 AW406187 231 AW406187 AW406187 232 AU0550644	22 ALG33127 154 BG516645 ALG33127 159 BF599554 BG516645 170 BF880060 BF880965 110 AW005961 AW005961 170 BF880064 BF880064 150 BF59553 BF59551 141 BF9596519	13 A901517 A8001517 II 110 AW001800 AW001800 WS 1 AA043001 AA043001 ZK56 22 A1559567 AISS9567 tq5	151 bp mRNA EST 01-DEC-2000  p-e-08-0-UI.s! NIH_BMAP_MHI2_S1 Mus musculus cDNA clone p-e-08-0-UI 3', mRNA sequence. GI:11524497  CI:11524497   Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
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RESULT 1 BF458328/C LOCUS . ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

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The IL-13 binding protein and related therapeutic molecules can be used in the antagonism of at least one IL-13 activity. They can be used for treating IL-13 mediated conditions such as certain allergic conditions such as asthma or to inactivate locally administered IL-13 after IL-13 treatment. The products can also be used as diagnostic agents, e.g. for detecting autoimmune diseases. The antibodies can also be used for immunotherapy and may also be used as a diagnostic tool.
                                              Claim 10; Page 46; 69pp; English.
  for diagnosis or detection
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Sequence 465 BP; 158 A; 79 C; 92 G; 135 T; 1 other;

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                                                                                                                                                                                                                                                                                                                        antiallergic; antiasthmatic; nootropic; neuroprotective; anticonvulsant; vulnerary; asthma; inflammation; allergy; Chediak-Higashi syndrome; CHS; Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes; digestion disorder; wound healing disorder; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                 Exocytosis pathway protein; Exo protein; antiparkinsonian; antidiabetic;
                     S
                  haemopoletin receptor protein family NRB gene. The sequence was used to isolate further mouse NRB genes. Antibodies to the NRB family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of
                                                                                                                                    Gaps
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         sequence represents a PCR amplified fragment of the mouse
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Pred. No. 1.8e+02;
3: Mismatches 0;
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                    Expropreting and their agonists and antagonists are useful in the diagnosis, treatment or prevention of exocytosis-mediated disorders such as asthma, inflammation, allergies, Chediak-Higashi Syndrome (CHS), Alzheimer's disease, Parkinson's disease, Huntington's disease, Intenders, digestion disorders and wound healing disorders. The nucleic acids, antagonists or agonists of Exo proteins are useful in gene therapy. The nucleic acids are also useful for generating transgenic or knock-out animals which can be used in the development and screening of therapeutically useful reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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vamp3, snap-23, and the rab family of proteins
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P-PSDB; AAW56255, AAW56256, AAW56257.
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expressed sequence tags (EST's) and are used in a 3' RACE (rapid expressed sequence tags (EST's) and are used in a 3' RACE (rapid mapplification of CDNA ends) reaction to amplify the novel ligand-binding receptor, Zcytor2, from humans and macaques. Zcytor2 is a receptor for cytokines (particularly interleukin-13) expressed on the surface of testicular cells, probably being involved in spermatogenesis. It can be used to detect ligands that promote proliferation and/or differentiation of such cells in cultures and may also be used to treat infertility.

Antagonists of this receptor may be used to characterise ligand-receptor interactions and as male-specific contraceptives. By blocking the action of IL-13, receptor antagonists and ligand-binding this receptor can also be used to modulate immune function, e.g. in allergy and asthma, as a diagnostic to determine circulating levels of ligand and also to isolate and purify ligands. Antibodies can be used to assay circulating receptor (an abnormal level may be indicative of disease such as cancer), for labelling cells that express the receptor, and therapeutically as
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                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding testis-specific cytokine receptor - useful for identification of ligands or antagonists, potentially for use as male contraceptives or for infertility treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                           Grant FJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.0%; Score 13.8; DB 18;
80.0%; Pred. No. 1.5e+02;
ive 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25 BP; 6 A; 1 C; 11 G; 7 T; 0 other;
                                                                                                                                                                           Foster DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 59; 79pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98JP-0314153.
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                                                                                                                                                                           Baumgartner JW, Farrah TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-2000 (first entry)
                                                                                                    (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RCTCCAYTCRCTCCA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 ACTCCACTCACTCCA
                                                                                                                                                                                                                                                                                WPI; 1997-470820/43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-NOV-1999;
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                                                                                                                                                                                                             O'Hara PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA61554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA61554/c
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The invention relates to chimeric proteins comprising the human Klotho protein fused to a human immunoglobulin (ABB1691-B11694), and to DNA sequences encoding them (AAA61542-A61545). It also relates to gene therapy vectors comprising DNA encoding the chimeric proteins of the invention, to detection and assay of molecules which interact with Klotho, to antibodies raised against the chimeric protein and to a chimeric protein sof the invention have antiarthritic and nephrotropic activity, and may be used for the treatment, prevention and diagnosis of disorders with which Klotho is associated, including kidney disease, cedema (dropsy) and arthritis. Sequences AAA61557 represent PCR primers used in an exemplification of the invention to generate and alpha chain and the hinge and part of the CH2 domain of the human Ig64 (immunoglobulin G4) heavy chain.
                                                                      Chimeric polypeptide containing klotho protein bound to an immunoglobulin for treatment and prevention of kidney disease, dropsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hemopoletin receptor protein family NR8 used for diagnosis of blood formation disorders - \,
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemopoietin receptor family; NR8; antibody; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 13.8; DB 21;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 71 BP; 16 A; 13 C; 25 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fragment of mouse NR8 sequence used as a probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   blood formation disorder; fusion protein; ds
              Kato Y, Nabeshima Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 7; Page 172-173; 176pp; Japanese
                                                                                                                                 Example 1; Page 89; 94pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ59255 standard; DNA; 330 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                              92.0%;
80.0%;
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98JP-0297409
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 GCTCCACTCACTCCA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RCTCCAYTCRCTCCA 15
              Nakamura K,
                                          WPI; 2000-376499/32.
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                                                                                                   and arthritis
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19-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ59255;
              Hanai N,
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/standard\_name= "single nucleotide polymorphism"

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12-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                        The probe AAV27166 and primers AAV27167-V27168 were used in a method of the invention to isolate NR6 a novel haemopoietin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism; pulmonary embolism; paternity test; ds.
cell survival; therapeutic; neuronal proliferation; drug screening; ss;
PCR; primer; amplification; Human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                            New isolated haemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 13.8; DB 19; Length 18; Pred. No. 1.4e+02; 3; Mismatches 0; Indels
                                                                                                                                                                                 Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y;
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human gene single nucleotide polymorphism #721.
                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 3 A; 8 C; 4 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                       Example 16; Page 66; 182pp; English.
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replace(11,T)
/*tag= a
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                                                                                                                                                   (AMRA-) AMRAD OPERATIONS PTY (DZIE/) DZIEGLEWSKA H E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.0%;
80.0%;
                                                                                                                               96AU-0002246
                                                                                                            97WO-GB02479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF95960 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-260970/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 12; Conserv
                                   Synthetic.
Homo sapiens.
                                                                                                                              11-SEP-1996;
                                                                 WO9811225-A2
                                                                                                           11-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18
                                                                                      19-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF95960;
                                                                                                                                                                                                    Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
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The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensize, patentity testing, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of the human gene SNPS shown in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                        McCarthy JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytokine receptor; ligand binding; testicular cell; spermatogenesis; infertility; antagonist; contraceptive; diagnostic; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human and macague 2 cytor2 cytokine receptor primer 269803.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Daley GQ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.0%; Score 13.8; DB 22;
80.0%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21 BP; 4 A; 2 C; 11 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                    Lander ES, Gargill M, Ireland JS, Bolk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.4e+3; Mismatches
                                                                                                                                                                                                                                                                                                                          (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Examples; Page 98; 242pp; English.
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                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                         26-JUL-2000; 2000US-0220947.
16-AUG-2000; 2000US-0225724.
                                                                                                                           07-SEP-2000; 2000WO-US24503
                                                                                                                                                                                           99US-0153357
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Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RCTCCAYTCRCTCCA 15
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WO200118250-A2
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                                                                                                                                                                                           10-SEP-1999;
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                                                            15-MAR-2001
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us-09-532-263-6.rng

BP.

(first entry)

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Hemopoietin receptor protein family NR8 used for diagnosis of blood
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                                                                                                                   AAZ90894/c
ID AAZ90894 standard; DNA; 16
                                                                                                                                                                                                                                                     Human NR8 gene probe #122
     1 RCTCCAYTCRCTCCA 15
                         15 ACTCCACTCGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   formation disorders
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                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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19-OCT-1998;
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                                                                                                                                                                           AAZ90894;
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haemopoietin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNYTGGAGY encoding the amino acid sequence Trp-Ser. Tha sequences AAZ59258-259300 and AAZ90816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAS59258-529300 and AAS90816-299925 represent specific examples of probe sequences used in the search. Aatibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the isolation of sequences encoding human haemopoletin receptor protein family NRB genes. The NRB family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding
                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                               Length 15;
                                                                                                                                                                                                                                                                     Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemopoietin receptor family; NRB; antibody; diagnosis; blood formation disorder; fusion protein; probe; ss.
                                                                                                                                                                                                                             92.0%; Score 13.8; DB 21;
80.0%; Pred. No. 1.4e+02;
1ive 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
                                                                                                                                                                         Sequence 15 BP; 3 A; 0 C; 8 G; 4 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ90893 standard; DNA; 15 BP
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98JP-0297409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human NRB gene probe #121
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                           1 RCTCCAYTCRCTCCA 15
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15 ACTCCACTCACTCCA 1
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Best Local Similarity
Thes 12; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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19-OCT-1998;
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Maeda M;

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               haemopoietin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid sequence TFP-Ser. The sequences AAZ59258-259300 and AAZ90816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
                                                                                                                                                                                                                                                                                                                                                                  Gaps
invention relates to the isolation of sequences encoding human
                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                           Score 13.8; DB 21; Length 16; Pred. No. 1.4e+02; 3; Mismatches 0; Indels
                                                                                                                                                                                                                                           Sequence 16 BP; 3 A; 0 C; 8 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemopoietin receptor primer 2057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                  92.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Best Local Similarity 80.0'
....hes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   1 RCTCCAYTCRCTCCA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 ACTCCACTCACTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV27168 standard;
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0;

Gaps

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92.0%; Score 13.8; DB 21; Length 15; 80.0%; Pred. No. 1.4e+02;

3; Mismatches

Conservative

Best Local Similarity Matches 12; Conserv

Query Match

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AAZ90848;

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The invention relates to the isolation of sequences encoding human haemopoletin receptor protein family NRB genes. The NRB family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZS9258-229300 and AAZ90816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NRB family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
                                                                                                                                                                                    Hemopoietin receptor protein family NR8 used for diagnosis of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hemopoietin receptor protein family NR8 used for diagnosis of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the isolation of sequences encoding human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemopoietin receptor family; NR8; antibody; diagnosis; blood formation disorder; fusion protein; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 13.8; DB 21;
Pred. No. 1.4e+02;
3; Mismatches 0;
                                                                    (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 BP; 3 A; 1 C; 8 G; 3 T; 0 other;
                                                                                                                                                                                                                                           Example 1; Page 42; 176pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.0%;
80.0%;
             98JP-0214720.
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ID AAZ90880 standard; DNA; 15
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Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RCTCCAYTCRCTCCA 15
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                                                                                                                                                                                                        formation disorders
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                                                                                                            Maeda M;
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             24-JUN-1998;
19-OCT-1998;
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                                                                                                             Nomura H,
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Pred. No. 1.4e+02;
3; Mismatches 0; Indels
                                                                                                        Haemopoletin receptor family; NR8; antibody; diagnosis; blood formation disorder; fusion protein; probe; ss.
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80.0%;
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98JP-0297409
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ID AAZ90864 standard; DNA; 15
                                 (first entry)
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                                                                    Human NR8 gene probe #76
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Matches 12; Conserv
                                                                                                                                                                   Homo sapiens
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                               24-MAY-2000
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AAZ90864;

Query Match

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Indels

Length 15;

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The invention relates to the isolation of sequences encoding human haemopoletin receptor protein family NR8 genes. The NR8 family sequences were initially yearched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ5928-259300 and AAZ90816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Raemopoietin receptor family; NR8; antibody; diagnosis;
blood formation disorder; fusion protein; probe; ss.
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Pred. No. 1.4e+02;
3; Mismatches 0;
                                                                                                 Score 13.8; DB 19;
Pred. No. 1.4e+02;
0; Mismatches 0;
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         Sequence 15 BP; 2 A; 7 C; 0 G; 3 T; 3 other;
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                                                                              92.0%; Sco.
100.0%; Pre
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80.0%;
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98JP-0297409
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ID AAZ90848 standard; DNA; 15
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Best Local Similarity 80.0
Matches 12; Conservative
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Best Local Similarity 100.
Matches 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer;
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                                                                                                                                                  coding for novel haemopoietin receptors, e.g. the murine interleukin-11 (IL-11) receptor alpha chain gene (AAT17868). Such receptors are defined by their ability to hybridise to the probes under medium stringency conditions.
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                                   5 Degenerate hybridisation probes (AAT17870-74) are based on a האימידיי איריהראידיי איריהראידי איריהראידיי איריהראידי איריה איריהראידי איריהראידי איריהראידי איריהראידי איריה איריה איריה איריהר
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                                                                                           conserved motif (AAR92812) found in haemopoietin receptors. T
probes are used in the identification and/or cloning of genes
                                                                                                                                                                                                                                                                                                                                                                                                               Length 15;
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Maeda M, Nash A, Nicola NA, Rakar S, Wills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Score 13.8; DB 17;
Pred. No. 1.4e+02;
0; Mismatches 0;
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Claim 12; Page 51; 87pp; English.
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Conservative 0;
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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AAZ90864
AAZ90880
AAZ90893
AAZ90894
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AAF95960
                                                  OM nucleic - nucleic search, using sw model
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Sa ( ()	- 4 <del>-</del> 4	Human NRBgamma 3' Human low adenosin Human adenosine re Novel haemopojetin DNA encoding a mur Mature interleukin Human interleukin	4445 60	Mouse orphan cytok Mouse cytokine rec Human DNAX soluble Sequence encoding Human IL-6 recepto cDNA encoding a hu Human HR-1 recepto
AAA61554 AAZ59255 AAA89731 AAV22698 AAZ94555	AATU4952 AAQ54831 AAV04437 AAQ54830 AAN90793 AAZ50746	AAZ59253 AAF20982 AAA34860 AAV27142 AAA46793 AAV22702 AAAV0701	AAC140288 AAC14829 AAV0448 AAV22701 AAT96784 AAZ59247 AAC22974 AAC23374	AA29457 AA294577 AA208861 AA203202 AAX99654 AAV04131
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c 12 c 13 c 14 c 15			0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	

## ALIGNMENTS

Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist; therapy; diagnosis; probe; hybridisation; ss. Haemopoietin receptor probe HYB1. (AMRA-) AMRAD OPERATIONS PTY LTD. BP 95WO-AU00578 94AU-0007902 94AU-0007901 AAT17870 standard; DNA; 15 (first entry) WPI; 1996-171612/17. WO9607737-A1. 05-SEP-1994; 05-SEP-1994; 05-SEP-1995; 21-MAY-1996 14-MAR-1996 Synthetic. Hilton DJ; AAT17870; П RESULT AAT17870 

Nucleic acid encoding haemopoietin receptor containing conserved amino acid motif esp. IL-11 receptor alpha chain - used for developing IL-11 (ant)agonists

Haemopoletin recep Human gene single Human and macaque

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Human NR8

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Gaps

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Indels

Length 1218;

19 others

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Submitted (13-DEC-2000) Department of Plant Pathology & Microbiology, Texas A&M University, 2132 TAMUS, College Station, TX 77843-2132, USA
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/protein_id="AA659895.1"
/do_xref="GI:12584945"
/translation="marPTPETGTAVRLLENVKYRDSNYTREERVENLQYAYNKAA AHFAQERQQQILKYSPRRLEASLRTIVGMVVYSWAKYSKELMADLSIHYTYTLILDDS EDDPHPQMLTYFDDLQSGNPQKHPWWMLVNEHFPNVLRHFGPFCSLNLIRSTLDFFEG
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NWWWWNDLMSFYKEFDDPRDQTSLVKNYVVSEGITLNQALEKLTQDTLQSSEQMWVV
FSQKDPKIMDTIECFWHGYITWHLCDNRYRLKEIYDRTKDIQTEDAMKFRFYEQAFK
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Stachybotrys chartarum
Stachybotrys chartarum
Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.
1 (bases 1 to 1227)
Peplow,A.W. and Beremand,M.N.
Unpublished
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Stachybotrys chartarum trichodiene synthase (TRI5) gene, complete
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326 c 316 g 264 t
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/strain="JS58-17"
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Pred. No. 8.6e+02;
3; Mismatches 0;
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Pred. No. 8.6e+02;
3; Mismatches 0
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join(<1. .469,545. .>1227)
/gene="TRI5"
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/gene="TRIS"
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Peplow, A.W. and Beremand, M.N.
Direct Submission
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AF329103.1 GI:12584944
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/db_xref="C1:1151069"
/db_xref="C1:1151069
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                       Direct Submission
Submitted (15-JUN-1995) Nancy Y. Ip, Department of Biology, The
Hong Kong University of Science and Technology, Clear Water Bay,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (24-MAX-1996) Clinical Diabetes and Nutrition Section,
National Institutes of Health, 4212 N. 16th Street, Phoenix, AZ
85016, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="ciliary neurotrophic factor receptor alpha
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Thompson.D.B., Ossowski,V., Sutherland,J., Apel,W. and Biesterfeildt,J.
Human Leptin Receptor
Unpublished
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Thompson, D.B., Ossowski, V., Sutherland, J., Apel, W. and
Biesterfeldt, J.
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Pred. No. 8.6e+02;
3; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                             /note="CNTF receptor alpha component"
/codon_start=1
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Human leptin receptor (LEPR) gene, exon
U59253.1 GI:1589760
J. Neurochem. 65 (6), 2393-2400 (1995)
96064819
                                                                                                                                                                                                                                                                          /organism-"Gallus gallus"
/db_xref="taxon:9031"
/tissue_type="brain"
/dev.stage="embryo"
1. 1089
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/db_xref="taxon:9606"
/chromosome="1"
/map="lp11"
550. 694
                                                                                                                                                                                                                             Location/Qualifiers
1. .1089
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80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
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Length 1227;

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cDNA encoding Ig-CRH region of human G-CSF receptor.
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/db_xref="taxon:9606"
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U29245
U29245.1 GI:1151068
                                                                                                                                                                                                                                                                                                        strandedness: Double;
topology: Linear;
hypothetical: No;
anti-sense: No;
                                                                                                                                                                                                                                                                                 C12R1:91),
(C12P21/02,C12R1:91);
                                                                                                                                                                                                        no sapiens (human)
1996140678-A/2
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Best Local Similarity 80.0
Matches 12; Conservative
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                                                     Homo sapiens (human)
                            JP 1996140678-A/2.
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     δ
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join(L38020.1:1. .152,L38021.1:21. .132,L38022.1:26. .110,
L38023.1:26. .259,L38024.1:26. .144,L38024.1:319. .484,
L38024.1:1555. .1758,26. .206,551. .719,809. .993)
/product="c11iary neurofrophic factor alpha receptor"
join(L38022.1:26. .110,L38023.1:26. .259,L38024.1:26. .144,
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                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 993)
Valenzuela,D.M., Rojas,E., Le Beau,M.M., Espinosa,R., Brannan,C.I., McClain,J., Masiakowski,P., Ip,N.Y., Copeland,N.G., Jenkins,N.A. and Yancopoulos,G.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MAAPVPWACCAVLAAAAAVVYAQRHSPQEAPHVQYERLGSDVTL
PCGTANWDAAVTWRVNGTDLAPDLLNGSQLVLHGLELGHSGLYACFHRDSWHLRHQVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LHVGLPPREPVLSCRSNTYPKGFYCSWHLPTPTYIPNTVLHGSKIMVCEKDPAL
KNRCHIRYMHLFSTIKYKVSISVSNALGHNATAITFDEFTIVKPDPENVVARPVPSN
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IIQVAAKDNEIGTWSDWSVAAHATPWTEEPRHLTTEAQAAETTTSTTSSLAPPPTTKI
                                                                                                                                                            Genomic organization and chromosomal localization of the human and mouse genes encoding the alpha receptor component for ciliary neurotrophic factor
                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/product="cillary neurotrophic factor alpha receptor"
/protein_id="AAA9137.1"
/db_xref="GI:608656"
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                                      ciliary neurotrophic factor alpha receptor.
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Pred. No. 8.5e+02;
3; Mismatches 0;
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65, Last updated, Version 2)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
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/note="non-coding exon"
                                                                                                                                                                                              Genomics 25 (1), 157-163 (1995) 95293367
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80.0%;
8-10, complete cds.
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L38025.1 GI:608654
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336 c
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/number=9
809. .993
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Matches 12; Conservative
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139 GCTCCAGTCACTCCA 125
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                                                                             Homo sapiens
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E11420/c
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AC E11420;
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DT 08-OCT-1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                            OLD Y., Hiraoka O., Anaguchi H.;
"DNA CODING FOR PROPEIN OF LIGAND-BONDING REGION CONTAINING CRH REGION OF
GRANULOCYTE COLONY STIMULATING PACTOR RECEPTOR";
PALENT number JP1996410678-A/2, 04-JUN-1996.
TANPAKU KOGAKU KENKYUSHO:KK.
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1 (bases 1 to 1089)
1 (bases 1 to 1089)
1 (bases 1 to alpha component of the chick ciliary neurotrophic factor receptor: developmental expression and down-regulation in
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15-NOV-1994 JP 1994280655
OTA YOSHIMI, HIRAOKA OSAMU, ANAGUCHI HIROYUKI
C12N15/09,C07H21/04,C07K14/715,C12N5/10,C12P21/02,(C12N5/10,
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09-JAN-1998

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LOCUS HUMCNFAR06 993 bp DNA PRI 09-JAN-2001
DEFINITION Homo sapiens ciliary neurotrophic factor alpha receptor gene, exons
                                                                                                                                                                                                                                                                                                                                Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 801).

Totases 1 to 801, W.K., Wu-Peng, X.S., Zhang, Y., Liu, S.M., Tartaglia, L. and Leibel, R.L. Phenctypes of mouse diabetes and rat fatty due to mutations in the OB (leptin) receptor Science 271 (5251), 994-996 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (22-DEC-1997) Pediatrics, Columbia University, 1150 St. Nicholas Avenue, New York, NY 10032, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chua.S.C., Koutras,I.K., Han,L., Liu,S.M., Kay,J., Young,S.J., Chua.S.C., and Leibel,R.L.
Chua,W.K. and Leibel,R.L.
Fine structure of the murine leptin receptor gene: splice site suppression is required to form two alternatively spliced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 (bases 1 to 801)
Chud,S.C., Koutras, I.K., Han, L., Liu, S.M., Kay, J., Young, S.J.,
Chung, W.K. and Leibel, R.L.
                                                                   Length 639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 others
                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                   Mus musculus leptin receptor (Lepr) gene, exon 6. AF039448
                           Sequence 639 BP; 135 A; 227 C; 174 G; 103 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94;
                                                                 Score 13.8; DB 45;
Pred. No. 8.3e+02;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 13.8; DB 94;
Pred. No. 8.4e+02;
3; Mismatches 0;
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 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"/strain="129/J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcripts
Genomics 45 (2), 264-270 (1997)
98008913
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                                                                                                                                                                                                                                                               AF039448.1 GI:2760934
                                                                 Query Match 92.0%;
Best Local Similarity 80.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="Lepr"
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80.0%;
                                                                                                                                                                                                                       801 bp
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606 GCTCCAGTCGCTCCA 592
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Best Local Similarity
                                                                                                                                                                                                                                                                                                         house mouse.
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LOCUS
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MUMULEPR06/c
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ACCESSION
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ORIGIN
                                                                                                                                                                                                                                                                                                                       ORGANISM
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AUTHORS
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MEDLINE
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SEGMENT
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                            ;
0
                                                                                                                                                                                              Gaps
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"DNA CODING PROTEIN BC IN LIGAND-BOUND REGION IN GRANULOCYTE COLONY
STIMULATING FACTOR RECEPTOR";
Patent number JP196131172-A/2, 28-MAY-1996.
TANPAKU KOGAKU KENKYUSHO:KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="CRH region of human G-CSF receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTA YOSHIMI, ANAGUCHI HIROYUKI
C12N15/09,C07H21/04,C07K14/715,C12N1/21,C12P21/02,(C12N1/21,
                                                                                                                                                                                           ö
                                                                                                                                                                 Length 639;

    639
    /note="CRH region of G-CSF receptor"

                                                                                                                                                                                            Indels
                                                                                                                         BP; 135 A; 227 C; 174 G; 103 T; 0 other;
                                                                                                                                                                Score 13.8; DB 45;
Pred. No. 8.3e+02;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA encoding CRH region of human G-CSF receptor
                                                                                                                                                                                                                                                                                                                                                                                                   07-0CT-1997 (Rel. 52, Created)
02-SEP-2000 (Rel. 65, Last updated, Version 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"/cell_line="U937"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="placenta"
1 .639
                                                                              /db_xref="taxon:9606"
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                    standard; RNA; HUM; 639 BP.

    .639
    /db_xref="taxon:9606"

                                        Location/Qualifiers
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14-NOV-1994 JP 1994278841
                                                                                                                                                                Query Match 92.0%;
Best Local Similarity 80.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            strandedness: Double;
topology: Linear;
hypothetical: No;
anti-sense: No;
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JP 1996131172-A/2
                                                                                                                                                                                                                                      606 GCTCCAGTCGCTCCA 592
                                                                    .639
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 misc_feature
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Gaps

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80.0%;
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Tris-HCl:
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                MgC12:
                                                             pH:
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Best Local Similarity
Matches 12; Conserv
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  Buffer:
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primer_bind
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                                                                                                                                   source
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G56634 620 bp DNA STS genomic, sequence tagged site.
                                                             RI
             2 (bases 1 to 597)
Coleman,A.W. and Mai,J.C.
Direct Submission
Submitted (15-AUG-1996) BioMed, Brown University, Providence, 02912, USA
ON VO. 10, 1997 this sequence version replaced gi:2039187.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 95 degrees C for 10 minutes
94 degrees C for 30 seconds
60 degrees C for 30 seconds
72 degrees C for 23 seconds
30
Perkin Elmer 9700
                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5801
Fax: (650) 320-5801
Email: olivier@hygo.stanford.edu
Primer A: TITCCTGCTGTTTTGTCCAAT
Primer B: GATTTCATCAGGTCCAGCAATTC
STS size: 281
                                                                                                                                                                                                                                                                                                                                              Score 13.8; DB 14; Length 597;
Pred. No. 8.2e+02;
3; Mismatches 0; Indels 0
                                                                                                                                                                       1. 199
//note="ITS1"
/product="internal transcribed spacer 1"
200. 358
/product="5.8s ribosomal RNA"
359. 597
/note="ITS2"
                                                                                                                                                                                                                                                                                                                                                                             Indels
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each 1 uM
each 200 uM
: 0.07 units/ul
5 ul
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Olivier,M. and Cox,D.R.
Unpublished, Olivier, M., Cox, D.R. (2000)
Unpublished (2000)
                                                                                                               1. .597
//organism="Chlamydomonas incerta"
//strain="SAG7.73"
/db_xref="taxon:51695"
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Amplifaq Gold Polymerase:
Total Vol:
                                                                                                                                                                                                                                                                                        142 g
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Polymerization:
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80.0%;
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G56634.1 GI:6121803
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Best Local Similarity 80.0
Matches 12; Conservative
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                                                                                                                                                                        misc_RNA
                                                                                                                                                                                                                                           misc_RNA
                                                                                                                 source
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ORIGIN
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                         AUTHORS
TITLE
JOURNAL
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VERSION
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TITLE
JOURNAL
COMMENT
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G56634/c
LOCUS
MEDLINE
                REFERENCE
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SOURCE
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1-639
Ota Y., Anaguchi H., Hiraoka O.;
"DNA CODING FOR LIGAND BOND RANGE PROTEIN OF GRANULOCYTE COLONY STIMULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                             ó
                                                     BAC ends sequenced at TICR from the RPC111 BAC library. Designed and developed at the Stanford Human Genome Center. Location/Qualifiers
                                                                                                                                                                                                                                             Gaps
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19 195227288-A/2
29-AUG-1995
30-MAY-1994 JP 1994116252
21-DEC-1993 JP 93P 321862
0TA YOSHIMI, AMAGUCHI HIROYUKI, HIRAOKA OSAMU
C12N15/O9/C12P21/O2,(C12N15/O9,C12R1:91),(C12P21/O2,C12R1:19);
strandedness: Double;
topology: Linear;
hypothetical: No;
anti-sense: No;
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0
                                                                                                                                                                                                                        Length 620;
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                                                                                                                                                                                                                      Score 13.8; DB 54;
Pred. No. 8.3e+02;
3; Mismatches 0;
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02-SEP-2000 (Rel. 65, Last updated, Version 2)
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/tissue_type="Placenta"
                                                                                                                                                                              ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FACTOR RECEPTOR";
Patent number JP1995227288-A/2, 29-AUG-1995.
TANPAKU KOGAKU KENKYUSHO:KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA encoding CRH region of G-CSF receptor
                                                                                                                                                                             193
                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
2.5 mM
50 mM
10 mM
8.3
                                                                                                                                                                complement(525. .547)
1 123 c 147 g
                                                                                                                                                                                                                                                                                                                                             standard; RNA; HUM; 639 BP
                                                                                                                               /clone_lib="Human"
267. .547
267. .289
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155
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CIU66950/c
                             RESULT 5
AF227555/c
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ORIGIN
                                                                    DEFINITION
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REFERENCE
                                                                                               ACCESSION
                                                                                                             VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                           AUTHORS
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KEYWORDS
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0
                              unc-5-immunoglobulin and thrombospondin type 1 transmembrane
protein (alternatively spliced) [Caenorhabditis elegans, variety
Bergerac, Genomic/mRNA, 387 nt, segment 6 of 9].
847165
847165.1 GI:258524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l (bases 1 to 387)
Leung Hagesteijn.C., Spence,A.M., Stern,B.D., Zhou,Y., Su,M.W.,
Hadgecock.B.M. and Culotti.J.G.
UNC-5, a transmembrane protein with immunoglobulin and
thrombospondin type 1 domains, guides cell and pioneer axon
migrations in C. elegans
Cell 71 (2), 289-299 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenBank staff at the National Library of Medicine created this entry (NCBI glubbsq 116678) from the original journal article. This sequence comes from Fig. 2.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.0%; Score 13.8; DB 96; Length 387; 80.0%; Pred. No. 8e+02; 0; Indels 0.
                                                                                                                                                                                                                                                                                                                        Length 373;
                                                                                                                                                                                                                                                                  others
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/db_xref="taxon:6239"
/variety="Bergerac"
107 g 90 t
                                                                                                                                                                                              /dev_stage="adult"
/note="derived from cDNA library"
                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                        92.0%; Score 13.8; DB 8;
80.0%; Pred. No. 8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans variety Bergerac.
Caenorhabditis elegans
                                                                                                                                                                                                                                       /note="microsatellite MCW111"
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                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                  102
                                                                                                                                                                                                                                                 /rpt_type=tandem
74 c 53 g
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             3 (bases 1 to 373) van der Poel, J.J.
                                                                                                                                                                                                                                                                                                                                                     Conservative
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307 ACTCCAATCACTCCA 321
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Matches 12; Conserv
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Matches 12; Conserv
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/note="membrane glycoprotein"
/codon_start=2
/codon_start=2
/product="interleukin-6 signal transducer receptor"
/product="interleukin-6 signal transducer receptor"
/protein_id="mapr3398.1"
/db_xref="G1:8132803"
/db_xref=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydomonas incerta internal transcribed spacer 1, 5.8S ribosomal U66950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (24-JAN-2000) California Regional Primate Research
Center. University of California-Davis, One Shields Avenue, Davis,
CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.

1 (bases 1 to 597)
Mai,J.C. and Coleman,A.W.
The internal transcribed spacer 2 exhibits a common secondary structure in green algae and flowering plants
J. Mol. Evol. 44 (3), 258-271 (1997)
                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Catarrhini; Cercopithecidae;
AF227555 457 bp mRNA PRI 01-JUN-2000
Macaca mulatta interleukin-6 signal transducer receptor (IL-6)
MRNA, partial cds.
AF227555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9544"
/cell_type="peripheral blood mononuclear cells"
<1. .>457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytokine Signal Transduction Genes from Rhesus Macaques
Unpublished
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Pred. No. 8.1e+02;
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                                                                                                                                                                                                                                                                                                       Macaca mulatta
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecinae; Macaca.
                                                                                                                                                                     AF227555.1 GI:8132802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="gp130"
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 457)
Arredondo, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 457)
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Best Local Similarity 80.0
Matches 12; Conservative
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                                                                                                                                                                                                                                                               rhesus monkey.
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Gaps

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Conservative

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1 RCTCCARTCRCTCCA 15

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Submitted (O'HAR-2000) E-mail contact: humquery@sanger.ac.uk
Marker stSG67529 (Primer A : AAAAGTGAAAGAGGGAAAGG; Primer B :
AAAACCCAACGGATGG; amplimer size : 141 bp) was developed from a
Single pass sequencing read from H.sapiens flow-sorted chromosome
9-12 random shear fragment, SC9-12pJ10F12. Vector : pUC18 Site :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chicken.

Gallus gallus

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

I (bases 1 to 373)

Ruyter-Spira,C.P., Crooijmans,R.P., Dijkhof,R.J., van Oers,P.A.,

Strijk,J.A., van der Poel,J.J. and Groenen,M.A.

Development and mapping of polymorphic microsatellite markers

Anim. Genet. 27 (4), 229-234 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 373)

Wuyter 'Spira,C.P.', de Koning,D.J., van der Poel,J.J.,

Crooijmans,R.P.', Dijkhof,R.J. and Groenen,M.A.

Developing microsatellite markers from cDNA: a tool for adding

expressed sequence tags to the genetic linkage map of the chicken

Anim. Genet. 29 (2), 85-90 (1998)
                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                   HSJ10F12 340 bp DNA STS 07-MAR-2000
STS from H.sapiens random shear fragment, sequence tagged site.
AL159451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L48909 373 bp mRNA VRT 23-FEB-2001
Gallus gallus clone CDNA42R microsatellite MCW111 sequence.
L48909
                                                                                                                                                                                                                                                                                                                    Further information : http://www.sanger.ac.uk/HGP/Chr10/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.0%; Score 13.8; DB 54; Length 340;
80.0%; Pred. No. 7.9e+02;
live 3; Mismatches 0; Indels 0
                                                                                                                                                                                 1 (bases 1 to 340)
Hunt, S., Sins, S., Willey, D., Carter, N. and Ross, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                         /clone="SC9-12pJ10F12"
/tissue_type="Lymphoblastoid cell line"
/clone_lib="SC9-12pJ"
44 c 77 q 87 t 1 attach
                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
                                                                                                            AL159451.1 GI:7210385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L48909.1 GI:13111695
                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RCTCCARTCRCTCCA 15
  1 RCTCCARTCRCTCCA 15
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48 GCTCCAGTCACTCCA 34
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              AF039448 Mus muscu
L38025 Homo sapien
E11420 cDNA encodi
                                                                                                                      AF133269 Drosophil
AF053926 Stachybot
                                                                                                                                                   M73238 Human cilia
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I50845 Sequence 2
                                                                                                                                                                                                                                                                           AB015706 Homo sapi
AF068615 Mus muscu
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BC005707 Mus muscu
                                                                              AF329103 Stachybot
                                                                                              Z48168 G.gallus mR
S54212 ciliary neu
                                                                                                                                                                                                                                                                                                                                                                         AB012290 Mus muscu
                                                                                                                                                                                                                                                                                                                                                                                                                              AJ224115 Mus muscu
D17444 Mouse mRNA
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AR019619 Sequence
AR070271 Sequence
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                                                       Gallus gall
                                                                                                                                                                                                      I12552 Sequence 1
I56052 Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF167719 Sus scrof
AJ308426 Bos tauru
                                                                                                                                                                                                                                   U09028 Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                         X55720 Human mRNA
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                                                                                                                                                              AR070290 Sequence
AR070290 Sequence
AR074863 Sequence
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
                                                                                                                                                                                                                                                                                                       Sequence 1
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                                                    U29245 Gallus
U59253 Human
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MUSSDFLIFR
HSGCSFRD
AF167719
BTA308426
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/db_xref="taxon:32644"
7 c 0 g
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A70377
              MUMULEPR06
                            HUMCNFAR06
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AB012290
MMU49110
BC005707
AF135119
                                        E11420
GGU29245
HLPR108
AF329103
                                                                                                                      AF133269
AF053926
HUMCNTFR
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AB015706
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A49472
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AR070290
AR074863
112552
156052
OCU09028
S80963
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AF041846
AR019619
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DEFINITION
ACCESSION
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ORIGIN
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
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RESULT A70377

SOURCE

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Gaps

Searched:

Sequence:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match Length DB
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                                                                               August 29, 2001, 19:51:55 ; Search time 1774.1 Seconds (without alignments) 130.780 Million cell updates/sec
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                   1344157 seqs, 7733874588 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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1 RCTCCARTCRCTCCA 15
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em_htg_hum1:*
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em_hum6:*
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Perfect score:
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A70377 Sequence 7
AL159451 STS from
L48909 Gallus gall
S47165 unc-5-immun
AF227555 Macaca mu
U66950 Chlamydomon
G56634 SHGC-102031
E09857 CDNA encodi

HSJ10F12 L48909 S47134S6 AF227555 C1U66950 G56634 E09857

989 4114 54

A70377 ΩI

Description

SUMMARIES

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This genomic DNA sequence is a fragment of the Mycobacterium fortiutum plasmid pAL 5000 which contains ORF2. This sequence is used in a method which results in the formation of Mycobacterium recombinant vaccines from compositions that provide a continuous source of protein to an animal and stimulate cellular immunity. Such compositions are used to stimulate cellular immunity (by inducing Th-1 cells or cytotoxic T lymphocytes), particularly as vaccines (live or dead) for treating and preventing diseases caused by intracellular pathogens (bacteria, viruses, rickettsia or protozoa), and also cancer, autoimmune diseases, allergy or downers spongiform encephalitis, in humans or animals. The vaccines are administered by injection, orally and masally. These compositions provide consistent and long-lasting immunity. Transformed cells used in method are retained within macrophages, blocking the killing methods may be included in the presented by the macrophage. Several immunogen may be included in the same vaccine and the Mycobacterium cells serve as adjuvant.
                                                                                                                                                                                                                                                  Recombinant non-pathogenic Mycobacterium as vaccines providing long term cellular immunity - useful against intracellular pathogens, cancer and autoimmune disease, and are retained in host macrophages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2096 BP; 348 A; 743 C; 670 G; 335 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 6; 120pp; English.
                        98WO-US06056.
                                                                97US-0042849.
                                                                                                              (CYTO-) CYTOCLONAL PHARM INC
                                                                                                                                                                                                         WPI; 1998-568277/48.
                     27-MAR-1998;
                                                                28-MAR-1997;
                                                                                                                                                            Labidi AH;
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1 RCTCCARTCRCTCCA 15

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Search completed: August 29, 2001, 20:16:42 Job time: 7423 sec

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Gaps

0;

92.0%; Score 13.8; DB 19; Length 2096; 80.0%; Pred. No. 2e+02; ive 3; Mismatches 0; Indels 0;

Query Match 92.0 Best Local Similarity 80.0 Matches 12; Conservative

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Matches

ò 셤 RESULT 13

AAQ83223,

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Vaccine; cellular immunity; Th-1 cell; cancer; cytotoxic T lymphocyte; treatment; prevention; disease; autoimmune; intracellular pathogen; BSE; allergy; bovine spongiform encephalitis; macrophage; immunogen; adjuvant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A DNA sequence (AAT14602) codes for a novel splice variant (AAR94576) human gpl30. The splice variant was initially detected during the morula to blastocyst transition stage of a human embryo. The splicing event removes the exon coding for the transmembrane domain causing a frameshift resulting in a novel C-terminus (see AAR94575). The splice variant gpl30 antegonises the action of certain growth factors and can be used to ensure correct development of preimplantation embryos, partic. for in vitro fertilisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    New splice variant of gpl30 lacking the trans-membrane domain -useful as an antagonist for growth factors esp. for ensuring correct development of pre-implantation embryos
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                                                                                                     Gp130; transmembrane domain; growth factor antagonist; embryo pre-implantation; in vitro fertilisation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.0%; Score 13.8; DB 17;
80.0%; Pred. No. 2e+02;
ive 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                (ISTF ) ARS APPLIED RES SYST HOLDING NV.
                                                                                                                                                                                                                                                                                                                                                                   Smith SK;
                                                                     Human gp130 splice variant gene.
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                                   (first entry)
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Best Local Similarity 80.0
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-188444/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium
                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                           WO9609382-A1
                                                                                                                                                                                                                                                             21-SEP-1995;
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                                   20-JUN-1996
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 AAT14602;
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Pred. No. 1.9e+02;
3; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The gene encoding human CNTFR was subcloned into bacterial expression vector pCP110. The resulting plasmid, pRPN151, encoded a recombinant, mature form of human CNTFR. Further manipulation of the coding region optimized expression of the gene in E. coll RFJ26, allowing production of useful amounts
                                                                                                                                                                                                                                                                                            CNTFR; ciliary neurotrophic factor receptor; cytokine; agonist; antagonist; signal transduction pathway; pRPN151; Escherichia coli; ds.
 Indels
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 Mismatches
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(SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig. 2a-2d; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    Jocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ihle JN, Stahl N, Yancopoulos GD;
                                                                                                                                                    AAQ83223 standard; cDNA; 1591 BP.
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m
                                                                                                                                                                                                                                                            Human recombinant mature CNTFR
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80.0%;
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289..1404
/*tag= b
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1170 GCTCCAGTCACTCCA 1156
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1170 GCTCCAGTCACTCCA 1156
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 Conservative
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                                   1 RCTCCARTCRCTCCA 15
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P-PSDB; AAR70147.
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Best Local Similarity
Matches 12; Conserv
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12;
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Gaps

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RESULT

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AAT14602/ ID AAT14

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                                              antinflammatory; antibocterial; antivital; antifungal; antirheumatic; antifinammatory; antibocterial; antivital; antifungal; antirheumatic; antifinammatory; and antianemic. The sequences can be used for determining pathological conditions associated with an OREX-associated disorder. The nucleic acids can be used to express OREX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, proliferative disorders, neurodegenerative disorders, osteoarthritis, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The CNTFR coding sequence can be incorporated into cells, cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNTFR; transgenic animal; motorneurone disease; trauma; muscular dystrophy; inflammation; amytrophic lateral sclerosis; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding CNTF receptors - useful in diagnosis, physiological study and treatment of CNTF-related disorders
osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                ;
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Pred. No. 1.9e+02;
3; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                           Sequence 1419 BP; 333 A; 436 C; 384 G; 265 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ciliary neurotrophic factor receptor-coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
289..1407
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/product= CNTFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Fig 2; 92pp; English
                                                                                                                                                                                                                                                                                                                                                           92.0%;
80.0%;
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90US-0532285.
91US-0676647.
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545 gctccagtcactcca 559
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01-JUN-1990;
28-MAR-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Davis S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ20195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
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CNTF has been cloned and syntheisized in eukaryotic as well as bacterial expression systems, as described in International Application No. PCT/U.S. 90/05241. The CNTF receptor (CNTFR or CNTFR or alpha) has been cloned and expressed in eukaryotic cells, as described in U.S. Patent Application Serial No. 07/700,677 and International Application No. PCT/US91/03896, filed June 3, 1991. The present invention relates to a stable CNTF/receptor complex which possesses a different mobility in native polyacrylamide gels than either purified fractions of CNTF or CNTFR.
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                             Sequence encoding human ciliary neurotrophic factor receptor (CNTF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell-free ciliary neurotrophic factor-receptor complex - for diagnosis and treatment of cell proliferation and differentiation disorders e.g. myeloid leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ip N;
Yancopoulos GD;
                                                                                                                                                 ó;
and organisms (e.g. E.coli) for the expression of the receptor protein, Monoclonal antibodies can be raised to the CNTF. The can be used as a probe to screen a library for clones encoding members of the family of molecules including IL-6 receptor.
                                                                                                                     Length 1591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 13.8; DB 14; Length 1591; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                        Ciliary neurotrophic factor; receptor; protein complex; ds
                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1591 BP; 289 A; 536 C; 473 G; 293 T; 0 other;
                                                                       Sequence 1591 BP; 289 A; 545 C; 465 G; 292 T; 0 other;
                                                                                                                     Score 13.8; DB 13;
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Davis S, Everdeen D, Squinto SP, Stahl N,
                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 289..1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 2; 122pp; English.
                                                                                                                                                                                                                                                                      AAQ39626/c
ID AAQ39626 standard; cDNA; 1591 BP.
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80.0%;
                                                                                                                     92.0%;
80.0%;
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92US-0865878.
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                                                                                                                                                                                              Query Match 92.0
Best Local Similarity 80.0
Matches 12; Conservative
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                                                                                                                                                                              1 RCTCCARTCRCTCCA 15
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAR37820
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1992;
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                                                                                                                                                                                                                                                                                                                  AAQ39626;
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agents capable of modulating the activity of IL-13 and related cytokines such as interleukin-4 for the treatment of allergy, asthma and other conditions relating to IgE. The genetic sequences can
                                                                                                                          Query Match
Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200058473-A2.
                                                      including NR4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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02-APR-1999;
05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                      08-FEB-2001
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                                                                                                                                                                                                                                                                                                           AAC76452;
                                                                                                                                                                                                                                                     RESULT 10
                                           also
                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequences (AAT66164 and AAT66165) respectively code for novel mouse and human haemoprotein receptors (AAW09821 and AAW09822) designated NR4 that comprise the interleukin-13 (IL-13) receptor alpha-chain. To obtain the mouse sequence (genomic DNA prepd. from embryonal stem cells was screened with oligonucleotides encoding an amino acid sequence (WSDWS) found in many haemoprotein receptors. The genomic clone was used isolate NR4 cDNA clones from WEHI-3B cells, peritoneal macrophage, bone marrow, skin and kidney libraries, and a composite sequence for mouse NR4 was produced. The availability of genetic sequences for NR4 permits the development of a range of
                            Gaps
                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding animal haemopoletin receptor which interacts with interleukin-13 - useful to treat asthma, allergy or condition
 Length 1193;
                                                                                                                                                                                                                                                                 NR4; haemoprotein receptor; interleukin-13 receptor; IL-13; cytokine; allergy; asthma; therapy; ss.
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                           Indels
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121..123
/*tag= d
/note= "bases 121-123 (nnn) code for an
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/*tag* e
/note* "bases 640.642 (nnn) code for an
                                                                                                                                                                                                                                       Mouse interleukin-12 receptor alpha chain NR4 DNA.
Score 13.8; DB 15;
Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unidentified amino acid"
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                           3; Mismatches
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61..1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 48-50; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicola NA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exacerbated by IgE production
                                                                                                                                                      AAT66164 standard; DNA; 1383
92.08;
              80.08;
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61..141
/*tag= b
142..1338
                                                                                                                                                                                                             (first entry)
                            12; Conservative
                                                                     1 RCTCCARTCRCTCCA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-259018/23.
              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_difference
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                                                                                                                                                                                                                                                                                                                                                                               sig_peptide
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                                                                                                                                                                                 AAT66164;
 Query Match
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                           Matches
                                                                                                                                         AAT66164/c
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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antiporiatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antianaemic; gene therapy; cancer; proliferative antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypotrension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                           Length 1383;
be used in prodn. of recombinant NR4 or fusion proteins
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                                                                                                                                                                                                                                                                                                        Indels
                                                                                                               Sequence 1383 BP; 416 A; 296 C; 315 G; 350 T; 6 other;
                                                                                                                                                                                                                           92.0%; Score 13.8; DB 18;
80.0%; Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                    3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC76452 standard; cDNA; 1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombosis; contraceptive; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0127607.
99US-0127636.
99US-0127728.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Rattus rattus.
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                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding ligand-binding region contg. the CRH region of granulocyte-colony stimulating factor receptor - useful in treptment of leukaemia resulting from proliferation of granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding cytokine-receptor-complementary region G-CSF receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G-CSF; granulocyte colony stimulating factor; receptor; leukaemia; over-proliferation; recombinant; vector; ds.
                                                                  Auto-antigen from synovial cells of rheumatoid arthritis patients binds to antibodies present in these patients, for diagnosis and prediction of the disease
                                                                                                                                     auto-antigen clone A, which can be used to diagnose and predict the development of RA by reaction with antibodies in biological specimens, e.g. sera, from patients.

RNA was isolated from synovial cells from a RA patient and used to construct a cDNA library. This was screened using IgG separated from the synovial fluid of a RA patient. Active clones were isolated in a cloning vector, and inserted into an expression vector for the transformation of E. coli NM522. Transformatis on culture express clone A peptide and follistatin related protein
                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                  Length 990;
                                                                                                                               present sequence encodes the rheumatoid arthritis (RA)
                                                                                                                                                                                                                                                                                                       Indels
                     Tanaka M;
                                                                                                                                                                                                                                                    Sequence 990 BP; 321 A; 190 C; 193 G; 286 T; 0 other;
                                                                                                                                                                                                                                                                                 Score 13.8; DB 18;
Pred. No. 1.9e+02;
3; Mismatches 0;
                   Osaki S,
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/note= "no stop codon"
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1..999
                  Osakada F,
                                                                                                        Claim 9; Page 38; 61pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                  92.0%;
80.0%;
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                                                                                                                                                                                                                                                                                 Query Match 92.0
Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                   942 ACTCCAGTCACTCCA 928
                                                                                                                                                                                                                                 into the culture medium.
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                   Nakao K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-316314/32.
                                    WPI; 1997-281030/25.
(KANF ) KANEKA CORP
                                               P-PSDB; AAW17859
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                   Kishimura M,
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Matches
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AAT35138 encodes a human protein of a ligand binding region of a G-CSF (granulocyte colony stimulating factor) receptor. The DNA and protein are used in the development and/or study of drugs which can be substituted for G-CSF. Such drugs are useful in the treatment of leukaemia resulting from granulocyte over-proliferation. The DNA may be expressed recombinantly to provide a high yield of the protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ciliary neutrophic factor; neurological disease; haemorrhage; tumor; trauma; infection; Alzheimer's disease; Creuzfeld Jakob disease; Down's syndrome; central nervous system; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             92.0%; Score 13.8; DB 17; Length 999; 80.0%; Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                             Sequence 999 BP; 207 A; 347 C; 276 G; 169 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat ciliary neutrophic factor-alpha DNA.
Claim 4; Page 12-14; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
81..1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ67887 standard; DNA; 1193 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Fig.1; 49pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94WO-US01057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RCTCCARTCRCTCCA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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28-OCT-1999.

Synthetic

AAZ43552;

AAZ43552

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This sequence represents the C-terminal domain of a ligand binding region of a human granulocyte colony stimulating factor (G-CSF) receptor. This sequence, the corresponding mouse sequence (see AAT33515) or a conserved fragment of both these sequences (see AAT33517) or an expression vector for the production of the receptor. The sequences can also be used in an expression vector containing E-coli maltose binding protein to produce a fusion protein. The DNA can be used in the study of diseases related to the interaction between the G-CSF receptor and its ligand, as well as for the treatment or prevention of G-CSF receptor ligand-binding region produced, is physiologically active and can be used in the study of the G-CSF receptor, such as analysis of its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.0%; Score 13.8; DB 17; Length 639; 80.0%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                          DNA coding for a ligand-binding region BC of G-CSF receptor useful for prevention or treatment of G-CSF diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rheumatoid arthritis; auto-antigen; clone A; diagnosis; prediction; synovial cell; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 639 BP; 135 A; 227 C; 174 G; 103 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA for rheumatoid arthritis auto-antigen clone A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
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                                                                                                                                                                                                                                        (TANP-) TANPAKU KOGAKU KENKYUSHO KK.
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1..990
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                                                                                                                                        94JP-0278841
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                P-PSDB; AAW00648.
Homo sapiens
                                              JP08131172-A.
                                                                                                                                                                                         14-NOV-1994;
                                                                                                                                            14-NOV-1994;
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                                                                                           28-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel method (A) of inducing differentiation of a bone marrow stromal progenitor cell to an osteoblastic lineage is new and comprises contacting the bone marrow stromal progenitor cell with an amount of leptin or its analog. The products of the invention have osteopathic activity. The method is useful for inducing differentiation of a bone marrow stromal progenitor cell to an osteoblastic lineage and for inducing bone formation in mammals. Therefore the method is useful for the treatment of osteoporosis and other conditions where bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        formation is required. This sequence represents a PCR primer used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Granulocyte colony stimulating factor; G-CSF; C-terminus; mouse; human; ligand binding domain; E.coli; maltose binding protein; receptor; G-CSF-dependent disease; G-CSF abnormality; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inducing differentiation of bone marrow stromal progenitor cells to an osteoblastic lineage \,\cdot\,
                                                                                                                                                                                                                                                            OB-R; leptin; PCR primer; differentiation; bone marrow; osteopathic; stromal progenitor; osteoblastic lineage; treatment; osteoporosis; ss.
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                                                                  BP.
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                                                                AAZ43552 standard; DNA; 22
                                                                                                                                                           21-FEB-2000 (first entry)
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Matches 12; Conservative
                                                                                                                                                                                                             Human OB-R PCR primer 2.
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                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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Query Match

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RESULT 5

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29-SEP-1998
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Zhang J;
                                                                                                                                                                                                                                                                                                                            Mammalian.
                                                                                                                                                                                                                                                                                                               Synthetic.
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                                                                                                                                                                                      AAV27138;
                                                                                                                                                                                                                                                                                        probe.
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                                                                                                                                                                                      Gaps
                     5 Degenerate hybridisation probes (AAT17870-74) are based on a conserved motif (AAR92812) found in haemopoietin receptors. The probes are used in the identification and/or cloning of genes coding for novel haemopoietin receptors, e.g. the murine interleukin-11 (IL-11) receptor alpha chain gene (AAT17868). Such receptors are defined by their ability to hybridise to the probes under medium stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide HYB2 hybridises under medium stringent conditions to a novel DNA (see AAT64442) encoding human haemopoietin receptor NR2 (AAW14841). It was used in the isolation of a partial NR2 sequence from a CDNA library constructed from the bone marrow mRNA of a patient recovering from chemotherapy. NR2 and genetic sequences encoding it can be used in the development of (ant)agonists, therapeutics and diagnostic reagents based on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human haemopoietin receptor NR2, and corresponding DNA - used e.g. for treatment of autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                             Haemopoietin receptor; new receptor 2; NR2; leptin; human; autolimune disease; nervous system; cerebral palsy; trauma induced paralysis; vascular ischaemia; stroke; neuronal tumour; motor neurone disease; Parkinson's disease; Huntington's disease; Alzheimer's disease; multiple sclerosis; peripheral neuropathy; heavy metal; alcohol; toxicity; kidney! fallure; infectious disease; herpes; rubella; measles; chicken pox; HIV; HTLV-1; therapy; probe; ss.
                                                                                                                                                           Length 15;
                                                                                                                                                                                                                                                                                                                                                                         Haemopoietin receptor NR2 hybridising oligonucleotide HYB2
                                                                                                                                                                                     Indels
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                                                                                                                                                          92.0%; Score 13.8; DB 17;
100.0%; Pred. No. 1.4e+02;
iive 0; Mismatches 0;
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                                                                                                                       Sequence 15 BP; 2 A; 7 C; 0 G; 3 T; 3 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ligand interaction with the receptor
Claim 12; Page 51; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMRA-) AMRAD OPERATIONS PTY LTD.
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                                                                                                                                                                                                                                                                                                  BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nicola NA, Willsont;
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                                                                                                                                                                                                                                                                                               AAT64433 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                           1 RCTCCARTCRCTCCA 15
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                                                                                                                                                           Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemopoietin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening; ss;
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The probes AAV27138 and AAV27139 are used to identify nucleic acid
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eda M, Nash A, Nicola NA, Rakar S, Willson T;
                     Length 15;
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                  Score 13.8; DB 18;
Pred. No. 1.4e+02;
0; Mismatches 0;
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100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel haemopoietin receptor probe 1.
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92.0%; Scc.
100.0%; Pre
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100.0%; Pic
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(DZIE/) DZIEGLEWSKA H E.
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T. Maeda M,
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GenCore version 4.5 Copyright (c) 1993 - 2000 Com	search, using sw model ust 29, 2001, 20:16:40 ; S	US-09-532-263-7 15 1 RCTCCARTCRCTCCA 15	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	30101 seqs, 313950809 residues		ength: U -ength: 200000000 Maximum Match 0% Maximum Match 100%	Geneseq_0601:* /SIDSB/gcgdata/geneseq//SIDSB/gcdata/geneseq//SIDSB/g		the number of results predi than or equal to the score by analysis of the total	SUMMARIES ry ch Length DB ID	0000000000
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sequence.

NA ALO24826

ALO24826.1 GI:3262169

GSS: genome survey sequence.

Takifugu rubripes.

ISM Takifugu rubripes.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Actinopterygii; Neopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Takifugu.

I (bases 1 to 360)

SS Elgark M., Smith,S., Meek,S., Warner,S., Umrania,Y., Williams,G. and Brenner,S.

Direct Submission

AL Submitted (O9-UTNI-1980) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB, UK. Email:

biohelp@hgmp.mrc.ac.uk

Vertor: pBluescript II KS
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Fugu rubripes GSS sequence, clone 006118bD2, genomic survey
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3; Mismatches 0; Indels 0;
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3; Mismatches 0; Indels 0;
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1. 360
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/db_xref="taxon:31033"
/clone="006118bb2"
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                                                         86 t
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/tissue_type="whole animal"
/dev_stage="varied"
1 69 c 74 g 86 t
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161 GCTCCAGTCGCTCCA 175
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Search completed: August 29, 2001, 19:22:13 Job time: 24136 sec

ORGANISM

REFERENCE

AUTHORS

TITLE JOURNAL COMMENT

FEATURES

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Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Pedoderinae; Caenorhabditis.
1 (bases 1 to 360)
Koharary', Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A. and Nishigaki,A.
Expression map of the C.elegans genome
Unpublished (1996)
                    Washington University School of MedicineP

Washington University School of MedicineP

4444 Forest park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1810

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:454254
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Pred. No. 2.4e+03;
3; Mismatches 0; Indels
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/db_xref="taxon:6239"
/clone="yk395h5"
                                                                                                                                                                                                                                                                                                                       Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 209. Location/Qualifiers 1. .355
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Tel: 81-559-81-6854
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib= Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH108"
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/db_xref="taxon:10090"
/clone="IMAGE:737206"
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Gene Library Lab
National Institute of Genetics
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Location/Qualifiers
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/db_xref="taxon:6238"
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/db_xref="taxon:6238"
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First strand oligo(dT) primed. Second strand was as per Gubler/Hoffman. Ligated to EoRI adaptors. Library is non-directional. Library is non-normalized. Library constructed by P.E. Kuwabara. Additional details on construction of the library are described in P.E. Kuwabara and S. Shah, NAR 22: 4414 - 4418 (1994). Adaptor sequence: GAATPIC GGTYGGTGGTG"
sequence: GAATPIC GGTYGGTGGTG"
                    Eukaryotta; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 352)
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR_F: TGTAAAACGACGCCAGTGAGCAAGTTCAGCCTGG
PCR_B: CAGGAAACGACGTGACGATATGAGTATTCTTCCAGGGTA
Source: Washington University Genome Sequencing Center
PCR amplified DNA is available from Washington University Genome
Sequencing Center. Aliquots of the library may be requested from P.
Kuwabara (pek@mrc-lmb.cam.ac.uk)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Location/Qualifiers
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Contact: Marra MA
Washington University Genome Sequencing Center
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Lnc 0; Indels

    352
    /organism="Caenorhabditis briggsae"

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The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mmarra@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA272591.1 GI:1910922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1455
Fax: 314 286 1810
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SOURCE
ORGANISM
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BASE COUNT ORIGIN

Matches

ò g ACCESSION

RESULT

TITLE JOURNAL

REFERENCE AUTHORS

; 0

Gaps

us-09-532-263-7.rst

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Senome Exploration Research Group, Life Science Tsukuba Center,
                                      Genome Science Laboratory
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                                                                                                  Sciences Center
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                                                                                                                                                                                                                                                                                                                                                     Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=QVI-BT0631-280
200-084-f01_Lis_1=2000-002-28&t4=1)
200-084-f01_Lis_2=2000-002-28&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 321.
Location/Qualifiers
1. .321
/Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BY0631"
/dev_stage="Adult"
/dev_sta
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S. Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hiozawa, M., Kadota, K., Kagawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, J., Kai, C., Kawal, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matayyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Shigemoto, Y., Shinaqawa, A., Sakai, C., Sato, K., Shibata, K., Shigemoto, Y., Shinaqawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiko, M., Muramatsu, M. and Hayashizaki, Y.

Nikin Mouse Ests (Konno, H., et al.)
Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                             Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                            Shotgun sequencing of the human transcriptome with ORF expressed
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Pred. No. 2.4e+03;
3; Mismatches 0; Indels 0;
                                                                  Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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                                                                                                                                                                 Contact: Simpson A.J.G.
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80.0%;
                                                                                                                                                                                                                                                                                                                                   rel: +55-11-2704922
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Best Local Similarity 80.0
Matches 12; Conservative
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Simpson, A.J.
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                            TITLE
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Email: genome-resertc.riken.go.jp,
UKL: http://genome.rtc.riken.go.jp,
UKL: http://genome.rtc.riken.go.jp,
Carninci,P. Nishiyama.Y., Westover,A., Itch,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itch,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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The Institute of Physical and Chemical Research (RIKEN), Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/db_xref="taxon:10090"
/db_aref="taxon:10090"
/clone=1a430092F05"
/clone_lib="RIKEN full-length enriched, 0 day neonate thymus"
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Pred. No. 2.4e+03;
3; Mismatches 0; Indels 0;
                                 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="0 day neonate"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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80.0%;
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MEDLINE COMMENT

JOURNAL

source

FEATURES

BASE COUNT ORIGIN

DEFINITION BB599621/c

RESULT

ó a ACCESSION KEYWORDS

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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Email: genome-resettc riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
Carninoi.P. Nishiyama.Y. Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
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cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 321)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silvay,W. Jr., Zago,M.A., Bordin,S., Coste,F.F.,
Ragai,M.A., A., Externatio,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepared by using trehalose thermo-activated reverse transcriptuse and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5
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/dev.stage="9 days embryo"
/lab_host="9 Hilbs"
/lab_host="9 Hilbs"
/note="Site="1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research forup in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Pred. No. 2.4e+03;
3; Mismatches 0; ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="b030001N11"
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Best Local Similarity
Matches 12; Conserv
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AUTHORS
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KEYWORDS
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S. Aizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P., Hanagaki, T., Hayatsu, N., Hiraoka, T., Hirozane, T., Hodoyama, Y., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Rawai, J., Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Oktazaki, Y., Okido, T., Owa, C., Sakai, C., Sakai, K., Sasaki, D., Sato, K., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. asunishi, A., Yoshida, K., Kontact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
                                                                                                                                                                                                 Tal: +55-11-2704922

Fax: +55-11-2707001

Bmail: asimpsoneluday.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MRI-CT0355-160 200-003-f04613=200-002-16644=1)

Seq primer: puc 18 forward: 20

High quality sequence start: 20
High quality sequence stop: 281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ONESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
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Pred. No. 2.4e+03;
3; Mismatches 0; Indels 0;
Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0355"
/dev_stage="Adult"
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Best Local Similarity 80.0
Matches 12; Conservative
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Eukaryotza Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 281)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                      trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation carninci, P. and Hayashizaki, Y.
Carninci, P. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5" of the primer of the pri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW859532 281 bp mRNA EST 19-MAY-2000
MR1-CT0355-160200-003-f04 CT0355 Homo sapiens CDNA, mRNA sequence.
AW859532
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                                                                                                                                                                                                                                                                           High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A730085006"
/clone_lib="RIKEN full-length enriched, 7 days neonate
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Pred. No. 2.4e+03;
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/dev_stage="7 days neonate"
/lab_host="DH10B"
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Best Local Similarity
Matches 12; Conserv
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AW859532/c
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URL:http://genome.rtc.riken.go.jp,
Carninci,P., Nishiyama,Y., Westover.A., Itch,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
                   Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/seq/gethtml.pl?tl=IL&t2=IL-BT161-010.html &t3=080399&t4=1)
Seq primer: puc 18 forward.
Location/Qualifiers
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The Institute of Physical and Chemical Research (RIKEN), Genomic
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Genome Exploration Research Group, Life Science Tsukuba Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 2.4e+03;
3; Mismatches 0; Indels 0;
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                                                                                                       1. 254
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT161"
/sex="female"
/dev_stage="Adult"
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BB258685.1 GI:8951518
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80.0%;
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Matches 12; Conservative
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Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carnhoci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. Akiyama,J., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. 463-470 (1999)
Carnhoci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 242) Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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MR1-CT0355-180200-006-c12 CT0355 Homo saplens CDNA, mRNA sequence.
AW859572
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80.0%;
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/Organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/done_lib="cq0355"
/dov2stage="Adult"
/note="Corgan: colon; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES POR (U.S. Letters Patent application No. 196
/716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue many and colnA amplification were performed under low
                                                                                                                                                                                                                                                                Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-MRl-CT0355-180 Seq primer: puc 18 forward
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Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Shotgun sequencing of the human transcriptome with ORF expressed
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IL-BT161-080399-010 BT161 Homo sapiens CDNA, mRNA sequence.
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Pred. No. 2.4e+03;
3; Mismatches 0; Indels 0;
                         sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
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High quality sequence stop: 242.
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58 c 40 g
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/organism="Homo
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Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Site_1: SalI: Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Expoloration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
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Kim T.O., Hong,Y.C., Yu,H.S., Hwang,M.Y., Yun,H.C., Kong,H.H. and Chung,D.I.
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Please visit our web site (http://genome.rtc.riken.go.jp) for
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Pred. No. 2.3e+03;
3; Mismatches 0; Indels 0;
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/dev_stage="adult"
/lab_host="DH108"
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51 ACTCCAGTCACTCCA 65
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. CE (Dases 1 to 232)

RS Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Iazawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Toya, Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Yano, R., Yano, R., Yananishi, A., Yokota, T., Yanahasa, I., Yano, R., Yananishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. (Dupublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-resertc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
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BB018457 RIKEN full-length enriched, adult male testis (DH10B) Mus
musculus cDNA clone 4930578B11 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Entamoeba histolytica trophozoite"
/dev_stage="trophozoite"
/lab host="x=0.blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
                                                                                                                                                                                  Email: dichung@bh.kyungpook.ac.kr
Submitted through BRIC(Biological Research Information Center) of
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Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
                                             Kyungpook National University School of Medicine
Dong-in dong 101, Chung-gu, Taegu 700 - 422, Republic of Korea
Tel: 82-53-420-6958
Fax: 82-53-422-9330
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Pred. No. 2.4e+03;
3; Mismatches 0; Indels
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Tel: +81-298-36-9013
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/clone="En044"
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Contact: Chung DI
Department of Parasitology
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BB018457.1 GI:8190064
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80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
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					FEATURE	108											BASE COL	ORIGIN		Query	Matche	<b>^</b> 0				RESULT BB189498	LOCUS	DEFINIT	ACCESSIC	KEYWORD	SOURCE		REFERENC AUTHOI				TITLE	COMMENT			
Description	Description	AW408083 UI-HF-BM0	BB189498 BB189498	A1002410 A1002410 BB018457 BB018457	AW859572 MR1-CT035	A1907996 IL-BT161-	BB258685 BB258685	AW859532 MRI-CT035 RR599621 RR599621	BE080913 OV1-BT063	BB209387 BB209387	R04486 pk24c12.rl	AA272591 va75c12.r	ALO24826 Fugu rubr	AV401050 AV401050	AV698306 AV698306 AA984710 am90a11 s	AW489097 UI-M-BH3-	BF760838 RC4-CT010	AA663262 aB8010/.S AQ060441 CIT-HSP-2	AV523125 AV523125	AV743168 AV743168 N75185 vw33a04 r1	BF706981 281663 MA	BG263/54 WHE2348_F AO663435 HS 2160 B	AQ332979 HS_5005_B	AQ667104 HS_2106_B AA619632 v154d09.r	AA082811 zn25a04.r	AA495324 fa01c03.r R73050 yj94f12.rl	AW279627 fj42c06.x m21805 3003 fambda	AZ151949 SP_0006_B	BF820788 MR1-RT004	AQ648347 RPC193-EC	AI311382 q088e12.x BF776672 287536 MA	AT005091 AT005091 BF200134 WHE2252 D	AQ668275 HS_2121_B		EST 16-FEB-2000 mo sapiens CDNA clone			Vertehrata. Puteleostomi.	Catarrhini; Hominidae; Homo.	I (bases 1 to 140) MH-MGC http://mgc.nci.nih.gov/. Nafional Institutes of Balith Mammalian Gone Collection (MC)	delle collection (Mac)
£		AW4 08083	BB189498	BB018457	AW859572	AI907996	BB258685	AW859532 BB599621	BE080913	BB209387	R04486	AA272591 C65054	FR0028454	AV401050	AV698306 AA984710	AW489097	BF760838	AA003202 AQ060441	AV523125	AV/43168 N75185	BF706981	BG263754 AQ663435	AQ332979	1 AQ667104 AA619632	AA082811	AA495324 R73050	AW279627 T21895	AZ151949	BF820788	AQ648347	AI311382 9 BF776672	AT005091 BF200134	AQ668275	ALIGNMENTS	140 bp mrnA ES: -d-10-0-01.rl NIH MGC_38 HOMO	A sequence.	<b>-</b>	Chordata. Crantata.	Primates; Catarrhini	i.nih.gov/. f Roalth Mammalian	r nearth, manualtan
E	- 1	115	127	123	121	103	129	121	163	128	187	156	222	30	22	116	169	223	31	159	168	231	227	231	~ ~	188	114	239	223	231	169	106	231		dq 0-0-0	E E	:692/140			c.nc	֝֝֞֝֟֝֝֞֝֝֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֡֝֜֝֓֓֓֓֡֝֓֓֓֡֓֜֝֡֓֡֓֡֝֝֓֡֓֡֝֜֝֡֡֡֝
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& Query Match		92.0	92.0	92.0	92.0	95.0	92.0	92.0	92.0	92.0	92.0	0.00	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0 92.0	92.0		AW408083 UI-HF-BM0-adu	IMAGE: 30628 AW408083	T. FRORO.	numan. Homo sapiens Eukarvota: M	Mammalia; Eutheria;	-MGC ht	tonat thitohou
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. CE [ bases 1 to 181]
RS Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Ishirawa, T., Ishikawa, J., Ishikawa, T., Itoh, M., Isaowa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, Y., Sujemoto, Y., Shinayawa, A., Shiraki, T., Sogabe, Y., Sujahara, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watanishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Riken Mouse ESTS (Konno, H., et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: prir3-pac; Site_1: Not1; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA Constructed from size fractionated cytoplasmic mRNA M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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The Institute of Physical and Chemical Research (RIKEN), Genomic
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musculus cDNA clone A330054L14 3', mRNA sequence.
Email: cgapbs-r@mail.nlh.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image.html

Seq primer: Ml3 Forward.
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Pred. No. 2.3e+03;
3; Mismatches 0; Indels 0;
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
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/organism="Homo sapiens"
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

gb\_gss33:\* gb\_gss34:\* em\_gss\_inv4:\* em\_gss\_rod6:\* em\_gss\_rod7:\* em\_gss\_rod8:\* gb\_gss35:\* gb\_gss35:\* gb\_gss37:\*

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em\_esthum10:\*
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em\_estov2:\*
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gb\_est30:\*
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gb\_est44: gb\_est45: gb\_est46: gb\_est47:

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gb\_est26: gb\_est27: gb\_est28: gb\_est29:

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                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   OM nucleic - nucleic search, using sw model
                                                                                                                                        August 29, 2001, 19:22:10
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qb_est39:*
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9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENRACYGGTYCICHMITREPSOTSIYQLDLWAGKQLLWNSSERFRSEHYKPPARRILTY
HADISHTWLLTWNNPYPSDNLLYSELTYLVNISNENDPTDFRTYNVTYMGPTLRVAAS
TLRSGASYSARVKAWAQSYNSSWSAWSPSTKWLNYYEDTWEQRLQLGYGISCVIVLAV
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                   AF081273 704 bp mRNA MAM 03-MAR-1999 Bos taurus interleukin-4 receptor alpha chain mRNA, partial cds. AF081273 GI:4322316
                                                                                                                                                                                                                                                                                                                                         Trigona, W.T. and Estes, D.M.

Trigona, W.T. and Estes, D.M.

Cloning of bovine homolog to interleukin-4 receptor alpha chain upublished

(bases 1 to 704)

Trigona, W.T. and Estes, D.M.

Direct Submission

Submitted (29-JUL-1998) Veterinary Pathobiology, University of Missouri-Columbia, 201 Connaway Hall, Columbia, MO 65211, USA

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .704
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/db_cref="taxon:9913"
/db_tref="peripheral blood activated T lymphocytes"
<1. .7704
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Pred. No. 2.1e+03;
2; Mismatches 1;
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80.0%;
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561 GCTCCACGCGCTCCA 547
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206 c 206 g 138 t
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HLDGEDVAMAHADALDDFDLDMLGDGDSPGFGFTPHDSAPYGALDMADFEFEQMFTDA
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                                                                                                                                                                                                                                                                                                                                                            0
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 701)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (16-FEB-2000) Graw J., Institute of Mammalian Genetics,
GSF-National Research Center for Environment and Health,
Ingolstaedter Landstr. 1, D-86764 Neuherberg, GERMANY
Location/Qualifiers
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Mus musculus mRNA for beta-A2-crystallin (cryba2 gene).
AJ272227
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Pred. No. 2.1e+03;
2; Mismatches 1; Indels (
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Pred. No. 2.1e+03;
2; Mismatches 1;
                                                                        /note="unnamed protein product"
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                                                                                                                                                                                                                                              119 t
                                                                                                          /protein_id="CAA03823.1"
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beta-A2-crystallin; CRYBA2 gene.
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64. .657
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80.0%;
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Best Local Similarity 80.0%;
Matches 12; Conservative
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Sequence 1 from Patent WO9730164.
A64741
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     88.0%;
80.0%;
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80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
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275 ACTCCAGGCGCTCCA 261
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291 GCTCCAGGCACTCCA 277
                                                                      1 RCTCCANGCRCTCCA 15
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                                                                                                                                                                                 /product="prolactin receptor"
/product="prolactin receptor"
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/db_xref="d1:999115"
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AGQOTBERKLSCHPGGXYVQYRCKPDHGYWSAWSPATFIQIPSAW"
164 c 154 g 159 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="beta-a2 crystallin"
/protein_id="bata0002.1"
/protein_id="bata0002.1"
/db_xref="di:16272.1"
/db_xref="di:16272"
/dene="beta-A2"
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1 (bases 1 to 696)

van Rens,G.L.M., Driessen,H.P.C., Nalini,V., Slingsby,C., de Jong,W.W. and Bloomendal,H.
Isolation and characteriation of CDNAs encoding beta-A4-crystallins: Heterologous interactions in the predicted dene 102, 179-188 (1991)
                                                                                                                                      <1. .621
/note="This sequence comes from Fig. 5; hPRL receptor"</pre>
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
entry [NCBI glbbsq 168377] from the original journal article. This sequence comes from Fig. 5.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                      Score 13.2; DB 97; Length 669; Pred. No. 2.1e+03;
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Cow beta-A2 crystallin (beta-A2) mRNA, complete cds.
M60329
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                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="BT474"
/cell_type="breast cancer"
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Bos taurus cDNA to mRNA.
Bos taurus
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/organism="Bos taurus"
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46. .639
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80.0%;
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BOVBA2/c
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30...623
/gene="CRYBA2"
/note="lens structural protein"
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VRSVKURGWWAPERFPFOEQGOFILERGOFFPRWSARGWASSSSHNSNOLLSFRPVLCAN
HNDSRYTLFEGDNFGGCFFPLVDDPFDSLPSMGWASKDVGSLKVSSGAWVAYQYPGYRG
YQYVLERDRHSGEFCTYGELGTQAHTGQLQSIRRVQH"
123 c 212 g 120 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (abses 1 to 700)
Wistow, G.
Direct Submission
                                                                                                                                                                                                                                                                               AF166331 700 bp mRNA PRI 22-JUL-1999
Homo sapiens beta crystallin A2 (CRYBA2) mRNA, complete cds.
AF166331
                                                              Gaps
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     Length 696;
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Haseloff.Jr. and Hodge,S.
Hareloff.Jr. and Hodge,S.
HareOvemenrs IN OR RELATING TO GENE EXPRESSION
Patent: WO 9730164-A 1 21-AUG-1997;
MEDICAL RES COUNTL. (GB)
Other publication AU 1801497 19970902.
Location/Qualifiers
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Pred. No. 2.1e+03;
2; Mismatches 1;
Score 13.2; DB 7;
Pred. No. 2.1e+03;
2; Mismatches 1;
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FEATURES
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Web: www.genoscope.cns.fr)
The CDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
CP 5706 91057 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
2 (bases 1 to 607)
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                                                                                                                                                                         Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation.
ALI14721 GI:5829340
      Gaps
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                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungl; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Sclerotiniaceae; Botryotinia.

1 (bases I to 607)

Bitton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y. Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
I (bases 1 to 60)
Fuh,G. and Wells,J.A.
Prolactin receptor antagonists that inhibit the growth of
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Pred. No. 2.1e+03;
2; Mismatches 1; Indels 0
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S78505
S78505.1 GI:999114
    Indels
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132 c 145 g 157 t 1 othe
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J. Biol. Chem. 270 (22), 13133-13137 (1995)
95286597
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      1;
      Mismatches
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Botryotinia fuckeliana.
Botryotinia fuckeliana
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    5,
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80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
    12; Conservative
                                           1 RCTCCANGCRCTCCA 15
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                                                     Direct Submission
Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
The CDNA library to be analyzed within the framework of this
project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant:
The library was produced in an oriented direction, in the PBSII
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Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
The cDNA library to be analyzed within the framework of this
project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant.
The library was produced in an oriented direction, in the PBSII
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Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
2 (bases 1 to 600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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BOLTYLIS cinerea strain T4 CDNA library under conditions of mitrogen deprivation.
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Helotiales; Sclerotiniaceae; Botryotinia.
1 (bases 1 to 600)
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132 c 143 g 158 t
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/organism="Botryotinia fuckeliana"
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2; Mismatches 1
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131 c 142 g 158
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CDM library; nitrogen deprivation.
Botryotinia fuckeliana.
Botryotinia fuckeliana.
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/db_xref="taxon:40559"
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16 ACTCCAAGCACTCCA 30
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The CDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
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Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
CP 5706 91057 EVRX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungl: Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Sclerotiniaceae; Botryotinia.

1 (bases 1 to 540)
Bitton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.
Direct Submission
Submitted (01-SEP-199) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
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(bases 1 to 600)

Bitton,F., Levis,C., Fortini,D., Pradler,J.M. and Brygoo,Y.

Direct Submission
Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
                                                 Gaps
                                                                                                                                                                                                                                     CNSOLD2D 540 bp mRNA PLN 03-SEP-1999
BOLTYLIS cinerea strain T4 CDNA library under conditions of nitrogen deprivation.
ALI16285 ALI16285.1 GI:5831501
CDNA library; nitrogen deprivation.
BOLTYOLINIA fluckellana.
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BOLTYPLIS cinerea strain T4 cDNA library under conditions of nitrogen deprivation.
ALI10729 ALI10729 ALI10729.1 GI:5825016
CDNA library; nitrogen deprivation.
BOLTYOCHINA fuckellana.
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/note="Genoscope sequence ID : W33E081"
120 c 133 g 135 t
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/organism="Botryotinia fuckeliana"
  Score 13.2; DB 14;
Pred. No. 2.1e+03;
2; Mismatches 1;
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Best Local Similarity 80.0
Matches 12; Conservative
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19 ACTCCAAGCACTCCA 33
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The CDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
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Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
CP 5706 91057 EVRX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (01-5EP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France 2 (bases 1 to 540)
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1 (bases I to $40)
Bliton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Botrytis cinerea strain T4 cDNA library under conditions of AL13767
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121 c 128 g 135 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 13.2; DB 9;
Pred. No. 2.1e+03;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                    1 (bases 1 to 357)
Kelly, P.A. and Nagano, M.
Soluble human prolactin receptors
Patent: US 6083753-A 3 04-JUL-2000;
Location/Qualifiers
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Botryotinia fuckeliana.
Botryotinia fuckeliana
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Sequence 3 from patent US 6083753.
AR102280
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90 c 76 g
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Best Local Similarity 80.0
Matches 12; Conservative
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317 ACTCCATGCACTCCA 303
                      317 ACTCCATGCACTCCA 303
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  Unclassified.
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BASE COUNT ORIGIN

FEATURES

25-MAY-1999

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2 (bases 1 to 172)
Hu,Z.Z., Zhuang,L., Meng,J.P. and Dufau,M.L.
Direct Submission
Submitted (16-SEP-1998) ERRB, NICHD, 9000 Rockville Pike, Bethesda,
MD 20892, USA
                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 172)
Hu,Z.S., Zhuang,L., Meng,J., Leondires,M. and Dufau,M.L.
The human prolactin receptor gene structure and alternative .
promoter utilization: the generic promoter hPIII and a novel human
                                                                                                                                                                       promoter hP(N)
J. Clin. Endocrinol. Metab. 84 (3), 1153-1156 (1999)
99182102
                                       HSPLRO7 172 bp DNA PRI HOMO sapiens prolactin receptor gene, exon 7. AF091867.1 GI:4886763
                                                                                                                                                                                                                                                                                 1. .172
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
16. .157
/number=7
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129 ACTCCATGCACTCCA 115
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M60329 Cow beta A2
AF166331 Homo sapi
A64741 Sequence
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BC006285 Homo sapi
AR101845 Sequence
AR102285 Sequence
AI411034 T7 end of
AX010400 Sequence
AR166329 Homo sapi
LOS561 Arabidopsis
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AF349939 Homo sapi
U03413 Dictyosteli
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D89016 Homo sapien
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A86031 Sequence 69
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Pred. No. 2.2e+03;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unidentified
unclassified.
1 (bases 1 to 108)
Haseloff,J.P. and Hodge,S.
IMPROVEMENTS IN OR RELATING TO GENE EXPRESSION
PATENT: MO 9730164-A 6 21-AUG-1997;
MEDICAL RES COUNCIL (GB)
Other publication AU 1801497 19970902.
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/db_xref="taxon:32644"
25 c 46 g 19
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Sequence 6 from Patent WO9730164.
                                                                                                                                                                     ATHPROKINA
AF107834
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AXOO6440
MMETL2912
MMU69491
                                                         AF081273
AX100243
A86031
                             AF166331
A64741
                                                 MMU272227
                                                                                      E66049
CNS01EU1
BC006285
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AX010400
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AF347936
CNS01BUX
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AF119386
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AR102285
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80.0%;
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A64746.1 GI:4530782
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Best Local Similarity 80.0
Matches 12; Conservative
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SOURCE
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                                                                                                                      Kelly, P.A. and Nagano, M. Soluble human prolactin receptors Patent: US 6083714-A 3 04-JUL-2000; Location/Qualifiers 1. 357
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ARI01840 357 bp DNA
Sequence 3 from patent US 6083714.
ARI01840 GI:12812638
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90 c 76 g
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                        August 29, 2001, 19:51:58; Search time 1774.1 Seconds (without alignments) 130.780 Million cell updates/sec
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                    1344157 seqs, 7733874588 residues
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Listing first 45 summaries
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AF091867 Homo sapi AR101840 Sequence AR102280 Sequence AL113767 Botrytis AL110729 Botrytis AL110779 Botrytis

A64746 HSPLR07 AR101840 AR10280 CRS01B4F CNS01B2D CNS01BS2 CNS01BS2

99 114 144 144

A64746 Sequence 6

Description

SUMMARIES

90-pr1:\*
90-pr2:\*\*
90-pr3:\*\*
90-pr3:\*\*
90-pr5:\*\*
90-pr7:\*\*
90-pr6:\*\*
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97US-097042B 96US-0012503 97US-0806597

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(ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV. (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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                                                                                                                                                                                          Kelly PA, Nagano M;
                                                                                                                                                                                                                     WPI; 2000-464346/40.
                                                                                                                                                                                                                                  P-PSDB; AAY95524.
                                                                                14-NOV-1997;
                                                                                                          29-FEB-1996;
26-FEB-1997;
                          US6083753-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                          Soluble human prolactin receptor (hPRLR) isoforms have been isolated from the extra- or intracellular domain and are thought to be generated by alternative splicing, since four clones (A, B, C and E) precisely lack alternative splicing, since four clones (A, B, C and E) precisely lack one or two exons. Except for clone C, the deletion in all other clones cresulted in a frameshift and produced a stop codon before the cransmembrane domain. The soluble hPRLR may be used as a binding protein for human prolactin and/or human growth hormone, which can be used in diagnostics for the detection and measurament of the binding ligand or in the rapeutics for binding to human prolactin and/or human growth hormone to retard or inhibit their hormone activities. They may also be used in the receptor sandwich or enzymatic assays, and in X-ray crystallographic analysis to develop molecular models, which define the certification and its receptor. This structure of the hormone-binding domains, where such information would provide insight into the structure of the actual contact between a hormone and its receptor. This structure information would be useful in the design of peptides which have prolactin or growth hormone-like
                                                                                                                                                                                                                 New soluble prolactin receptors useful as human growth hormone binding protein and in x-ray crystallographic analysis for developing molecular models which define the tertlary structure of the hormone-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 13.2; DB 21; Length 357;
Pred. No. 3.3e+02;
2; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding soluble isoform of human prolactin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 357 BP; 99 A; 90 C; 76 G; 92 T; 0 other;
                                                                                                        (INRM ) INSERM INST NAT SANTE & RECH MEDICALE. (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
                                                                                                                                                                                                                                                                                     Disclosure; Column 25-28; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prolactin receptor; human; isoform;
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                                                    97US-0806597.
                                                                               96us-0012503
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Matches 12; Conservative
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317 ACTCCATGCACTCCA 303
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                                                                                                                                                                                         P-PSDB; AAY96916.
                                                    26-FEB-1997;
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US6083714-A
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The present sequence is that of DNA encoding a newly identified soluble isoform of the human prolactin receptor (PRLR). The DNA lacks exons 5 and 6 of the full-length receptor, resulting in a lacks exons 5 and 6 of the full-length receptor, resulting in a saking the putative produces a stop codon before the transmembrane domain, the receptor. 6 Isoforms (see AAY95524) of human PRLR were the recembinant DNA molecules encoding the soluble PRLRS are provided, as well as expression vectors and host cells. The soluble PRLRs may be used as binding proteins for human prolactin and/or human growth hormone, which can be useful in diagnostics for the detection and measurement of the binding ligand, or in therapeutics for human prolactin and/or human growth hormone activities. They may also be used in place or inhibit their hormone activities. They may also be used in place of inhibit their hormone activities. They may also be used in place of inhibit their hormone activities.
New recombinant DNA having a segment encoding a signal peptide joined translationally to a segment encoding a soluble human prolactin receptor useful as a hormone growth hormone binding protein, and in x-ray crystallographic analysis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor assays, in receptor sandwich or enzymatic assays, and in x-ray crystallographic analysis to develop molecular models that define the tertiary structure of the hormone-binding domains, where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    such information would provide insight into the structure of the actual contact between a hormone and its receptor. This structural information would be useful in the design of peptides that have
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                                                                                                                                                                                                                                             Claim 8; Column 25-28; 27pp; English.
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Matches 12; Conservative
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6 gctccaagcactcca
                                                                        Chlamydia pneumoniae
                                                                                                                                                                                                            WPI; 1999-357842/30.
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                                                                                                                            20-NOV-1998;
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                                                                                                                                             04-NOV-1998;
                                                                                                          03-JUN-1999
                                                                                                                                                                                          Griffais R;
                                                               Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                         haemopoletin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ59258-Z59300 and AAZ9025 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as binding to the proteins are used for the treatment of such disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                   Gaps
                                                                                                                                                                                                                                                                                                                                                      The invention relates to the isolation of sequences encoding human
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 Length 15;
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                  Indels
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                                                                                                                                                                       Haemopoietin receptor family; NR8; antibody; diagnosis; blood formation disorder; fusion protein; probe; ss.
Score 13.2; ·DB 21;
Pred. No. 2.6e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 13.2; DB 21;
Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                    (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 3 A; 1 C; 7 G; 4 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 44; 176pp; Japanese.
                                                                                               AAZ90895 standard; DNA; 15 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.0%;
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88.0%;
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98JP-0297409.
                                                                                                                                   (first entry)
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                                                                                                                                                     Human NR8 gene probe #123.
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Thes 12; Conservative
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15 ACTCCATGCACTCCA
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Query Match
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                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                   WO9967290-A1
                                                                                                                                                                                                                                                       23-JUN-1999;
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19-OCT-1998;
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                                                                                RESULT 12
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AAX91991-X97517 represent PCR primers used to amplify open reading frames and other nucleic acid sequences from the genome of chlamydia pneumoniae (see AAX91940). C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema endosum or pharynquitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAX34584-AAX35879) can be used in immunogenic compositions as vaccines. Vectors conclaining c. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                        Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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primer used to amplify an ORF of Chlamydia pneumoniae.
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80.0%; Pred. No. 2.7e+02;
ive 2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= hPRLR_clone_B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 1496; Disclosure; 1912pp; English.
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97FR-0014673.
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Sequence 15 BP; 3 A; 1 C; 7 G; 4 T; 0 other;
            Example 1; Page 43; 176pp; Japanese.
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98JP-0297409
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                                                                                                                                                                                                    Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                        1 RCTCCANGCRCTCCA 15
                                                                                                                                                                                                                                                     15 ACTCCAGGCACTCCA 1
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                                                                                                                                                                                                                                                                                                                                                                     Score 13.2; DB 21;
Pred. No. 2.6e+02;
                                                                                            CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
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                                                                                                                                                                                                    Example 1; Page 42; 176pp; Japanese.
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80.0%;
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98JP-0297409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human NRB gene probe #105
                                                                                                                                                                                                                                                                                                                                                                               Query Match 88.0
Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              1 RCTCCANGCRCTCCA 15
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15 ACTCCAGGCACTCCA 1
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                                                                                                                   Maeda M;
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                                  23-JUN-1999;
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           29-DEC-1999
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                                                                                                                   Nomura
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    The invention relates to the isolation of sequences encoding human haemopoietin receptor protein family NRB genes. The NRB family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AST35128 escapence AST35128 espesent specific examples of probe sequences used in the search. Antibodies to the NRB family proteins are used for the diagnosis of blood formation disorders. Compounds identified
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encoding human
NR8 famil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.0%; Score 13.2; DB 21;
80.0%; Pred. No. 2.6e+02;
ive 2; Mismatches 1;
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24 - MAY - 2000
                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                Nomura H,
                                           AAZ90861;
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ID AAZ908
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            AAZ90861/c
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sequences used in the search. Antibodies to the NRB family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
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                                                                                               Gaps
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                                                                        Score 13.2; DB 21;
Pred. No. 2.6e+02;
2; Mismatches 1;
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Pred. No. 2.6e+02;
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                                          Sequence 15 BP; 3 A; 1 C; 7 G; 4 T; 0 other;
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80.0%;
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                                                                        Query Match 88.0
Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                         Human NR8 gene probe #65
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15 ACTCCATGCACTCCA 1
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Matches 12; Conserv
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The invention relates to the isolation of sequences encoding human haemopoietin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAAS9258-259300 and AAS90816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
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  BP.
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                                                                                                                                                      Human NR8 gene probe #89.
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les 12; Conservative
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AAZ90861 standard; DNA;
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15 ACTCCATGCACTCCA
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haemopoletin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNVTGGAGY encoding the amino acid sequence Trp-Ser. The sequences AA259258-259300 and AA290816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
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                                                                                                                                                                                                                                                                            protein family NR8 used for diagnosis of blood
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            Haemopoietin receptor family; NR8; antibody; diagnosis;
                        blood formation disorder; fusion protein; probe; ss
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Pred. No. 2.6e+02;
2; Mismatches 1;
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                                                                                                                                                                                               CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC
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80.0%;
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                                                  Homo sapiens
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blood formation disorder; fusion protein; probe; ss.
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80.0%; Pred. No. 2.6e+02;
ive 2; Mismatches 1;
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15 ACTCCAGGCACTCCA 1
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             Maeda M;
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Matches 12; Conserv
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               The invention relates to the isolation of sequences encoding human haemopoieth receptor protein family NRB genes. The NRB family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences ARS29288-259300 and AAS290816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NRB family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
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80.0%; Pred. No. 2.6e+02;
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ID AAZ59267 standard; DNA; 15
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Best Local Similarity 80.0
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88.0%; 80.0%;

Query Match Best Local Similarity

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15 ACTCCATGCACTCCA 1
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                               730101 segs, 313950809 residues
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                                                                                   August 29, 2001, 20:16:42;
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Maximum Match 100%
Listing first 45 summaries
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AAZ90872
AAZ90877
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Maximum DB seq length: 2000000000
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Hemopoietin receptor protein family NR8 used for diagnosis of blood formation disorders -  $\,$ 

WPI; 2000-116933/10.

Example 1; Page 38; 176pp; Japanese.

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Tel: 81-298-36-9145
Fax: 81-298-36-9016
Fax: 81-298-36-9016
Email: genome-res@ttc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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Musmalais Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalais Eutheria Rodentia; Sciurognathi; Murinae; Mus.

1 (bases 1 to 177)

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,

Akahira, S., Akiyama, J., Fukudaka, S., Fukunishi, Y., Funayama, T., Hara

A., Hayatsu, N., Hori, F., Ishikawa, T., Nitsuma, H., Oda, H., Owa, C.,

Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Suzuki, H., Tomaru, Y., Suzuki, H., Yamamura, T., Yokota, T., Tominaga, N.,

Mutanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,

Muranatsu, M., Okazaki, Y. and Hayashizaki, Y., Yoshino, M.,
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Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Matanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Musamatsu, M., Sata Maramatsu, M., Riken Mouse ESTs
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AV081754 Mus musculus stomach C57BL/6J adult Mus musculus CDNA
clone 2210421D01, mRNA sequence.
AV081754 GI:5213202
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/db_xref="taxon:10090"
/clone="2200005J24"
/clone_lib="Mus musculus stomach C57BL/6J adult"
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Pred. No. 4.8e+03;
2; Mismatches 1; Indels 0:
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
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/dev_stage="adult"
54 c 32 q
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                                                                                                                                                                    Genome Science Laboratory
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Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                Chie Owa
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Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):20-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455.3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
Location/Qualifiers
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//db_xrain="257BL/6J"
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//dc_stage="adult"
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clone 2200005H20, mRNA sequence.
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Contact: Chie Owa
Genome Science Laboratory
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S Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Alzawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukudishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Shigemoto, Y., Shireki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamanura, T., Yokota, T., Yoshino, M., RIKEN Wuse ESTS.

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Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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AV072630 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
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Pred. No. 4.8e+03;
2; Mismatches 1; Indels 0;
Score 13.2; DB 109; Length 171; Pred. No. 4.8e+03; 2; Mismatches 1; Indels 0;
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="2200007C09"
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Contact: Chie Owa
Genome Science Laboratory
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53 ACTCCAGGCGCTCCA 67
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                      Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
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AV072630
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305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9145
Fax: 81-298-36-9196
Fax: 81-298-36-9196
Fax: 81-298-36-9196
Fax: 81-298-36-9196
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):320-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                (bases 1 to 174)

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akıpanı, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Taceno, M., Tomaru, Y., Suzuki, H., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y., Yoshino, M.,
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Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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AV072658
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/clone_lib="Mus musculus stomach C57BL/6J adult"
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Pred. No. 4.8e+03;
2; Mismatches 1;
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/db_xref="taxon:10090"
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/dev_stage="adult"
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                                                                                                                                                      (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwWd2 (gil4722114(gblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIOGold (Stratagene) cells and selected for ampicillin resistance."
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Fax: 81-298-36-9145
Exa: 81-298-36-9198
Exa: 81-298-36-9198
Exai: 81-298-36-9198
Exai: 81-298-36-9198
Exai: genome-res@ttc_riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by trehablose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:

Mammalia: Eutheria; Rodentia: Sciurognathi: Muridae; Murinae; Mus.

1 (bases 1 to 166)

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,

Akahira, S., Akiyama, J., Eukudas, S., Eukunishi, Y., Funayama, T., Hara

A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,

Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C.,

Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Soqabe, Y., Sugahara, Y., Suzuki, H., Tarteno, M., Tomaru, Y., Tominaga, N.,

Matanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,

Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
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                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
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AV073140 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
clone 2200008009, mRNA sequence.
AV073140
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Pred. No. 4.8e+03;
2; Mismatches 1; Indels 0;
'clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                          Laboratory Mouse DNA Resource
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80.0%;
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Best Local Similarity 80.0%
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Unpublished (1999)
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62 ACTCCAGGCACTCCA 48
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Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Itoh, M., Izawa, M., Kawai, J., Sato, K., Shibata, Y., Shigamoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watranabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., RIKEN Mouse ESTS
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1. .166
/organism="Mus musculus"
/strain="C57BL/6J"
/db.zref="taxon:10090"
/clone="2200008009"
/clone="1b"="Mus musculus stomach C57BL/6J adult"
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/sex="male"
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
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    .171
    /organism="Mus musculus"

                                                                                                                                                                   /sex="male"
/tissue_type="stomach"
/dev_stage="adult"
49 c 33 g
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/clone="2210021D15"
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/dev_stage="adult"
53 c 32 q
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Contact: Chie Owa
Genome Science Laboratory
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18 ACTCCAGGCGCTCCA 32
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71 GCTCCATGCACTCCA 85
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1 (bases 1 to 162)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deolivelra, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shiqamoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Ruramatsu, M., Okazaki, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE069562 162 bp mRNA EST 09-JUN-2000 RC2-BT0389-090300-012-f12 BT0389 Homo sapiens CDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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50 c 30 q
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                                                                                                                          Contact: Chie Owa
Genome Science Laboratory
RIKEN
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BE069562.1 GI:8414212
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Fax: +55-11-2707001
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44 ACTCCAGGCGCTCCA 58
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1. .162
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/dev_stage="Adult"
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/716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

51 a 33 c 37 9 41 t
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC2-BT0389-090
300.012-fl2&t3=2000-03-09&t4=1)
Seq primer: puc l8 forward
High quality sequence start: 44
High quality sequence start: 44
High quality sequence stop: 162.
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Contact: Robert B. Welss
Contact: Robert B. Welss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 164)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Slam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ376266 164 bp DNA GSS 02-OCT-2000 MD130J006F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0130J06 F, DNA sequence. AZ376266
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Tel: 801 585 7156
Tel: 801 585 717
Tel: 6dunn@genetics.utah.edu
Insert Length: 10000 Std Error:
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42 ACTCCAGGCGCTCCA 56
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E 1 (bases 1 to 160)

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akipama, J., Fukuda, S., Fukudishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Isawa, M., Gwai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Itoh, M., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., RIKEN Mouse ESTS

L Unpublished (1999)
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Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998)) blease visit our web site (http://genome.rtc.riken.go.jp) for further details.
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AV074451 Mus musculus stomach C57BL/6J adult Mus musculus CDNA
clone 2210009E18, mRNA sequence.
AV074451
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             Score 13.2; DB 109; Length 159;
Pred. No. 4.7e+03;
2; Mismatches 1; Indels 0;
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
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               Query Match 88.0
Best Local Similarity 80.0
Matches 12; Conservative
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Best Local Similarity 80.0
Matches 12; Conservative
                                                                                          1 RCTCCANGCRCTCCA 15
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47 ACTCCAGGCGCTCCA 61
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AV074451
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E Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E I (bases 1 to 161)

S Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Alzawa,K., Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawal,J., Kikuchi,N., Kojima,Y., Matuyama,T., Itoh,M., Izawa,M., Kawal,J., Kikuchi,N., Kojima,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N., Watanabe,S., Yagame,M., Yamamara,Y., Yokota,T., Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

I Unpublished (1999)

Contact: Chie Owa

Genome Science Laboratory
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Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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AV074715 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
clone 2210010H07, mRNA sequence.
AV074715
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AV072831 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
clone 2200006M08, mRNA sequence.
AV072831
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/clone="2210010H07"
/clone="11b="Mus musculus stomach C57BL/6J adult"
/sex="male"
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Pred. No. 4.7e+03;
2; Mismatches 1; Indels 0;
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
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/organism="Mus musculus"
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/dev_stage="adult"
42 c 32 q
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80.0%;
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Fax: 81-298-36-9098
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Best Local Similarity 80.0
Matches 12; Conservative
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20 ACTCCAGGCGCTCCA 34
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Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Yarateno, M., Tomanatu, Y., Tominaga, N., Matanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
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Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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                                                                                                   Email: genome-resertc.riken.go.jp
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further details.
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                                                                                                                                                                                                                                                                                                                                                       /strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Pred. No. 4.7e+03;
2; Mismatches 1; Indels 0;
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                        3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
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                                                                                                                                                                                                                                                                                                               1. .135 // /Organism="Mus musculus"
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41 c 26 q
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Genome Science Laboratory
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80.0%;
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                                                             Tel: 81-298-36-9145
Fax: 81-298-36-9098
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Unpublished (1999)
Contact: Chie Owa
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Best Local Similarity 80.0
Matches 12; Conservative
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16 ACTCCAGGCGCTCCA 30
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Thermostabilization and thermoactivation of thermolabile enzymes by Thermostabilization and thermoactivation of the synthesis of full length cDNA trehalose and its application for the synthesis of full length cDNA Transcriptional Sci. U.S.A. 95(2):520-524 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))

Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 159)

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,

Ak, Hayatsu, N., Akiyama, J., Tukuda, S., Tukunishi, Y., Funayama, T., Hara

A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,

Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C.,

Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara

Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N.,

Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,

Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
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AV072952
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/db_xref="taxon:10090"
/clone="220007101"
/clone_lib="Mus musculus stomach C57BL/6J adult"
                                                                                                                                /clone_lib="Mus musculus stomach C57BL/6J adult"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                        88.0%; Score 13.2; DB 109;
80.0%; Pred. No. 4.7e+03;
iive 2; Mismatches 1;
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1. .13/
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41 c 27 q
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/dev_stage="adult"
51 c 27 q
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Contact: Chie Owa
Genome Science Laboratory
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Stamova, B. and Tong, J.C. The structure and function of the expressed portion of the wheat qenomes - Early reproductive apex CDNA library from Triticum	monococcum Unpublished (2001)	Contact: Olin Anderson US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773	Fax: 5105595818  Email: oandersn@pw.usda.gov  Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratagene SK primer.		<pre>/db_xret="taxon:4568" /clone="WHE2480_H02_004" /clone=lib="Triticum monococcum early reproductive apex cDNA library" /tissue_type="Early reproductive apex"</pre>	/dev_stage="Seven week-old plants" /lab_host="E. cold XLOLR" /note="Vector: Landda Uni ZAP XR, excised phagemid; /note="Vector: Landda Uni ZAP XR, excised phagemid; site_1: EcoRI; Site_2: XhoI; The tissue, total RNA, and	poly(a) NAM were prepared from apex at double-fruge stage to terminal-spikelet stage during transition from vegetative state to flower state, a cDNA library was made, and the cDNA clones were in vivo excised at the		13 a 47 c 46 g 13 t	/ Match 88.0%; Score 13.2; DB 155; Length 119; Local Similarity 80.0%; Pred. No. 4.7e+03; hes 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	RCTCCANGCRCTCCA 15 :        :       GCTCCATGCACTCCA 83		AV080202 135 bp mRNA EST 25-JUN-1999 AV080202 Mus musculus stomach C57BL/6J adult Mus musculus cDNA clone 2210413F10, mRNA sequence.	AV080202 AV080202.1 GI:5211650 EST.	house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	. (UGSP. 1.C) 132) Carnioci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Alzawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,	Arkuchi, N., Nojima,Y., Matsuyama,T., Niltsuma,H., Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Fateno,M., Tomaru,Y., Tominaga,N., Watanabe,S., Yaqame,M., Yamamura,T., Yokota,T., Yoshino,M., Muramatsu,M. Okazaki,V. and Havashisaki,V.	RIKEN Mouse ESTS Unpublished (1999) Contact: Chie Owa
TITLE	JOURNAL	COMMENT		FEATURES Source			•		BASE COUNT ORIGIN	Query Match Best Local Matches 1:	Oy 1 F	RESULT 2 AV080202	LOCUS	ACCESSION VERSION KEYWORDS	SOURCE ORGANISM DEFEDENCE	AUTHORS		TITLE JOURNAL COMMENT
SUMMARIES	DB ID Description	155 BG607593 BG607593 109 AV080202 AV080202 109 AV081442 AV081442 109 AV072952 AV072952	109 AV07415 AV07415 109 AV077415 AV07415 109 BE069562 BE069562 242 AZ376266 AZ376266	109 AV073140 109 AV076989 109 AV072886 109 AV072630	109 AV072638 AV072638 109 AV081754 AV081754 109 AV058439 AV088439 219 CNSO0TGF AL089661 109 AV077479 AV077479	109 AV072558 AV072558 109 AV077821 AV0771821 109 AV0771830 AV077830 145 ED146275 ED146278	109 AV072870 109 AV072872 109 AV088929	109 AV072097 AV072090 109 AV073900 AV073900 109 AV077817 AV077817	12 AAB40811 AAB40811 174 BG141411 BG141411 138 BE670421 BE670421 00 AV072587 AV072587	109 AV072779 109 AV072787 109 AV072799 109 AV074114	109 AV072750 AV072750 5 AA319785 E. 107 AU071883 AU07183 AU071883 AU071883 AU071883 AU071883 AU071883 AU071883 AU071883	109 AV077480 AV077480 109 AV078355	ALIGNMENTS	,	119 bp mRNA EST 17-APR-2001 42S Triticum monococcum early reproductive apex cDNA um monococcum cDNA clone WHE2480_H02_004, mRNA	GI:13657576	cum. iplantae; Streptophyta; Embryophyta; Tracheophyta; agnollophyta; Liliopsida; Poales; Poaceae; Pooldeae	119) Chao,S., Dubcovsky,J., Echenique,V., Han,P.S., Hsla Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L.,
σP	Query e Match Length	0.0000	0.000 0.000 0.000 0.000	00000	0.0000	000000	00000	0.000	0000	9 8 8 8 8 9 0 0 0 0 0	2 88.0 234 2 88.0 240 2 88.0 240 2 88.0 240 2 88.0 241	88.0 88.0			102_00 'ritic	G607593.1 G607593.1 ST.		Anderson, O.D., C.C., Kang, Y.,
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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em\_esthum22:\*
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August 29, 2001, 19:22:13 ; Search time 3770.35 Seconds (without alignments) 37.607 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Lindahl,M., Timmusk,T., Rossi,J., Saarma,M. and Airaksinen,M.S. Expression and alternative splicing of mouse Gfra4 suggest roles in endocrine cell development
                                                                                                                                                                                                                                                                    /translation="MSTSSHACPVPAVRGHWTHYPAAPYPLLFPPVIRGLSLPPLHGL
HGHPPPSGCSTPSPASVGQACQRTTGGSQFAASTKWTPSLNAAIE"
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Alzakainen,M.S.
Dirack Submission
Submitted (20-MAR-2000) Airaksinen M.S., Program in Molecular
Neurobiology, Institute of Blotechnology, P.O. Box 56 (Viikinkaari
9), 00014 University of Helsinki, FINLAND
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AJ276872.1 GI:7688070 alternative splicing; GDNF family receptor alpha 4; Gfra4 gene.
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Mus musculus mRNA for GDNF family receptor alpha 4, putative
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446. .526
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Pred. No. 1.7e+03;
2; Mismatches 1;
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527. .>534
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Mus musculus
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/gene="Girad"
//gene="Girad"
//gene="Girad"
//gene="Girad"
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//groduct="putative GDNF family receptor alpha 4, secreted
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//db_
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See also X56569, X56573, X56574 for Murine RAR-beta isoforms. Data kindly reviewed (18-FEB-1991) by Chambon P. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (08-NOV-1990) Chambon P., IGME/CRNS- U184/INSERM - Institute de Chimie Biologique, 11 rue Humann, 67085
STRASBOURG-Cedex, France
(Dases 1 to 534)
Zelent,A., Mendelsohn,C., Kastner,P., Krust,A., Garnier,J.M., Ruffenach,F., Lercy,P. and Chambon,P.
Differentially expressed isoforms of the mouse retinoic acid receptor beta generated by usage of two promoters and alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAR-beta gene; retinoic acid receptor; retinoic acid receptor beta
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 534)
Chambon, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Mouse RAR-beta mRNA for retinoic acid receptor-beta 3 isoform.
X56574
                                                                                                                                                                                                                                                                                                                         BAC end sequences from L. Hood at University of Washington. Designed and developed at the Stanford Human Genome Center. Location/Qualifiers
 60 degrees C for 30 seconds
72 degrees C for 23 seconds
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Perkin Elmer 9600
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each 1 uM
each 200 uM
: 0.07 units/ul
5 ul
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Pred. No. 1.7e+03;
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/organism="Mus musculus"
/db_xref="taxon:10090"
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50 mM
10 mM
8.3
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91114714
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82. .286
                 Polymerižation:
                                       PCR Cycles:
Thermal Cycler:
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Total Vol:
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80.0%;
   Annealing:
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Best Local Similarity 80.0
Matches 12; Conservative
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                                                                                               Template:
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                                                                     Echinometra.

1 (bases 1 to 450)
Pallumbi,S.R., Grabowski,G., Duda,T., Geyer,L. and Tachino,N.
Speciation and population genetic structure in tropical Pacific sea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="HPEVYILILPGFGMISHVIAHYSGKREPFGYLGMVYAMIAIGVL
GVLWAHHMFTVGMDVDTRAXXXAATMIIAVPFGIKVFSWMAXLOGSNIOWETPLFWA
LGFVFLFTLGGLTGIVLAMSIDVVLHDTYYVVAHFHYVXSMGAVFAI"
103 103 125 t 12 others
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 477)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G36845 477 bp DNA STS 31-DEC-1997
SHGC-60507 Human Homo sapiens STS genomic, sequence tagged site.
G36845
Echinometra mathaei.
Mitochondino Echinometra mathaei
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinosea; Echinoida; Echinometridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                Evolution 51 (5), 1506-1517 (1997)
2 (bases 1 to 450)
Palumbi,S.R., Grabowski,G., Duda,T., Geyer,L. and Tachino,N. Direct Submission
Submitted (12-AGC-1997) OEB, Harvard University, 16 Divinity Avenue, Cambridge, MA 02138, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Initial incubation: 95 degrees C for 10 minutes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 degrees C for 30 seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259689
Fax: 4157259689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 13.2; DB 5; Length 450;
Pred. No. 1.7e+03;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="cytochrome oxidase subunit I"
/protein_id="AAB69575.1"
/db_xref="G1:2353672"
                                                                                                                                                                                                                                                                                                                       /organism="Echinometra mathaei"
/organelle="mitochondrion"
/isolate="Nu4"
/db_xref="taxon:31178"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: myers@shgc.stanford.edu
Primer A: GCTGCCGACAGACAGTTTG
Primer B: ATGCAGCATGAAGCATGGAG
STS size: 205
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Richard M. Myers
                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/transl_table=9
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80.0%;
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Unpublished (1997)
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137 ACTCCAAGGACTCCA 123
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Matches 12; Conserv
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/gene="casr"
/gene="casr"
/gene="casr"
/gene="casr"
/product="calcium-sensing receptor"
/product="calcium-sensing receptor"
/product="calcium-sensing receptor"
/db_xref="c1:718864"
/translation="APKSRKLPENFNEAKFITFSMLIFFIVWISFIPAXASTYGKFVS
AVEVIALLAASFGLLACIFPNKYYIILEKPSNATIEEVRCSTAAHAFKVAARATLRRS
AVEVIALLAASFGLLACIFSSSKSNSEDPFPQP"
149 c 103 g 82 t
                                                                                                                                                                                                                                                          AF221064 413 bp mRNA ROD 07-MAR-2000
Meriones unguiculatus calcium-sensing receptor (CaSR) mRNA, partial
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                                                                                                                                                                                                                                                                                                                                                                          Meriones unguiculatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 413)
Mangemenn, P. and Scofield,M.A.
Direct Submission
Submitted (04-JAN-2000) Pharmacology, Creighton University, 2500
California Plaza, Omaha, NE 68178, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 413)
Wonneberger K., Scofield, M.A. and Wangemann, P.
Evidence for a calcium sensing receptor in the vascular smooth muscle cells of the spiral modiolar artery
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/db_xref="taxon:10047"
/tissue_type="spiral modiolar artery; kidney"
<1. .>413
                                                                  Length 396;
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                                                                  Score 13.2; DB 97
Pred. No. 1.8e+03;
2; Mismatches 1
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Pred. No. 1.8e+03;
2; Mismatches 1
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 107
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AF221064.1 GI:7188643
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Best Local Similarity 80.0
Matches 12; Conservative
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121 ACTCCATGGACTCCA 107
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343 GCTCCACGGGCTCCA 357
 96
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/protein_id="AAA16747.1"
/db_xref="G1:404797"
/translation="MG10GGSVLFGLLLVLAVFCHSGNSLQCYSCPLPTMESMECTAS
TNCTSNLDSGLIAKAGSGVYYRCWRFDDCSFKRISNQLSETQLKYHCCKKNLCNVKEV
LENGGTTLSKKTILLLVTPFLAAAWSRHP"
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Mammalia, Eutheria, Primates, Platyrrhini, Cebidae, Cebinae,
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Rother, R.P., Rollins, S.A., Fodor, W.L., Albrecht, J.C., Setter, E.,

Fleckenstein, B. and Squinto, S.P.

Inhibition of complement-mediated cytolysis by the terminal

complement inhibitor of herpesvirus saimiri

J. Virol. 68 (2), 730-737 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAICD59A 396 bp mRNA PRI 14-MAR-1994
Saimiri sciureus complement regulatory protein (CD59) mRNA,
CCMplete cds.
L22859
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                                                                                                    07-0CT-1997
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Pred. No. 1.8e+03;
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                                                                                                                                                                                                                                   1 (bases 1 to 396)
Fodor, W.L. Rollins, S. and Squinto, S.P.
Chimeric complement inhibitor proteins
Patent: US 5627264-A 6 06-MAY-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Saimiri sciureus"
/db_xref="taxon:9521"
/cell_line="DPSO 114/74"
/tissue_type="lung"
/tissue_lib="ATCC CCL194"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                      149083 396 bp DNA
Sequence 6 from patent US 5627264.
149083
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Salmiri sciureus.
Salmiri sciureus
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96 c 95 g
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                                                                                                                                                                                                                                                                                                                                                                                                                          88.0%;
80.0%;
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               121 ACTCCATGGACTCCA 107
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Best Local Similarity
Matches 12: Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unclassified.
1 (bases 1 to 396)
Fodor,W.L., Rollins,S. and Squinto,S.P.
Nucleic acid encoding chimeric complement inhibitor proteins
Patent: US 5624837-A 6 29-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                     (pases 1 to 396)
Rother,R., Rollins,S. and Squinto,S.P.
Terminal complement inhibitor fusion proteins
Patent: US 5847082-A 3 08-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAT
                                                                                                                                                                                                                                                                                               PAT
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Pred. No. 1.8e+03;
2; Mismatches 1;
                                                                                                                       Score 13.2; DB 94;
Pred. No. 1.8e+03;
2; Mismatches 1;
 HGHPPPSGCSTPSPATIETOSTSSEELVPS"
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Sequence 3 from patent US 5847082.
AR064381
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141335
141335.1 GI:2081925
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96 c 95 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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96 c 95 g
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                                                              6
                317. .>360
/gene="RAR-beta"
/note="exon 4"
                                                             80
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80.0%;
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80.0%;
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80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
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Best Local Similarity 80.0
Matches 12; Conservative
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Best Local Similarity 80.C
Matches 12; Conservative
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258 ACTCCATGGGCTCCA 272
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121 ACTCCATGGACTCCA 107
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Unclassified.
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FEATURES
                                                             BASE COUNT
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JOURNAL
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VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                        δλ
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/product="retinoic acid receptor- beta 1 isoform"
/protein_id="AaA39918.1"
/db_xref="MGD.MG1-7877"
/db_xref="MMGD.MG1-7877"
/db_xref="SWISS-PROT:P22605"
/translation="MSTSSHACPVPAVRGHWTHYPAAPYPLLFPPVIRGLSLPPLHGL
                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                       MMRARB1 360 bp mRNA ROD 16-APR-1991 X56569 1000se RAR-beta mRNA for retinoic acid receptor-beta 1 isoform. X56569 1 GI:53901 RAR-beta gene; retinoic acid receptor; retinoic acid receptor beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91114714
See also X56569, X56573, X56574 for Murine RAR-beta isoforms. Data
kindly reviewed (18-FEB-1991) by Chambon P.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 360)
Zelent,A., Mendelsohn,C., Kastner,P., Krust,A., Garnier,J.M.,
Ruffenach,F., Leroy,P. and Chambon,P.
Differentially expressed isoforms of the mouse retinoic acid
receptor beta generated by usage of two promoters and alternative
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (08-NOV-1990) Chambon P., LGME/CRNS- U184/INSERM
Institute de Chimie Biologique, 11 rue Humann, 67085
STRASBOURG-Cedex, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'product="retinoic acid receptor- beta 1 isoform"
                                                                                                                                                                                                   ó
                                                                                                                                                                    Length 325;
                                                                                                                                                                                                     Indels

    .325
    /organism="Drosophila melanogaster"
/strain="Oregon R"
    /db_xref="taxon:7227"
    /clone="128B5"

                                                                                                                                                                   Score 13.2; DB 54;
Pred. No. 1.8e+03;
2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. 360
/organism-"Mus musculus"
/db_xref="taxon:10090"
/chromosome="14A"
/cell_line="F9, P19"
date_of_search = 15-12-1995.
   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBO J. 10 (1), 71-81 (1991)
                                                                                                       75 g
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/gene="RAR-beta"
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/gene="RAR-beta"
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/note="exon 1"
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                      1 isoform.
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COMMENT
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FEATURES

TITLE

TITLE

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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              /organism="Mus sp.
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in_situ_site_primary = 54F
BLAST_program = BLASTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fruit fly.
Drosophila melanogaster
TANPAKU KOGAKU KENKYUSHO:KK.
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80.0%;
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Z71056.1 GI:1263558
                                                                                                                strandedness: Double;
topology: Linear;
hypothetical: No;
                                                                                                       (C12P21/02,C12R1:19);
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Best Local Similarity 80.0
Matches 12; Conservative
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294 GCTCCAGGGGCTCCA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RCTCCANGGRCTCCA 15
                        Mus sp. (mouse)
JP 1996131172-A/3
                                                                                                                                                     anti-sense: No;
                                               28-MAY-1996
                                                                                                                                                                                                                        mat_peptide
                                                                                           C12R1:19)
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ORGANISM
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DM128B5S
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Rođentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA encoding mouse ligand-binding region protein(BC) of G-CSF receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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"DNA CODING PROPERING C IN LIGAND-BOUND REGION IN GRANULOCYTE COLONY
"STRUCLATING FACTOR RECEPTOR";
Patent number JP1996131172-A/3, 28-MAY-1996.
                                                                                                                                                                                                                                                                                                                          Prepared with primer pairs derived from 238906 -- dbEST.
Location/Qualifiers
1. .310
/organism="Homo sapiens"
33. .309
bind 33. .52
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 310;
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9 Cambridge Center, Cambridge MA 02142 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13.2; DB 54;
Pred. No. 1.8e+03;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-0CT-1997 (Rel. 52, Created)
02-SEP-2000 (Rel. 65, Last updated, Version 2)
                                                                                                                                                                                                                                                                                                                                                                                                            81
                                                                                                                                                                                                                      Tag Polymerase: 0.025 units/ul
                                 Email: thudson@genome.wi.mit.edu
                                                                                                                Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                50 309)
50 9
                                                        Primer A: AAAACAAAAACGCGATGA
Primer B: CCTTGACCCACCTTGAGAGA
STS size: 277
PCR Profile:
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80.0%;
                                                                                                                                                                                   Template: 10 ng
Primer: each 5 pk
dNTPs: each 4 nM
                                                                                                                                                                                                                                                                   MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCL: 10 mM
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          Tel: 617 252 1900
Fax: 617 252 1902
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211 ACTCCAGGGGCTCCA 225
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Best Local Similarity
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                                                                                                                                                                            Protocol
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ID E11372
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1-324
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ORIGIN
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1 (bases 1 to 325)
European Drosophila Mapping, Consortium.
Direct Submission
Submitted (15-APR-1996) Michael Ashburner, Department of Genetics, Downing St., Cambridge CB2 3EH, England
stronger = Da12885
STS_from_promoter = SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D. melanogaster STS determined from European Mapping Project cosmid, sequence tagged site.
14-NOV-1994 JP 1994278841
OTA YOSHIMI, ANAGUCHI HIROYUKI
C12N15/09,C07H21/04,C07K14/715,C12N1/21,C12P21/02,(C12N1/21,
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database_version = 45.0 and updates till date_of_search
date_of_search = 08-01-1996
BLAST_program = BLASTX
database_searched = SWISSPROT
database_version = 32.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                        /product="mouse ligand-binding region protein(BC) of G-CSF receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13.2; DB 45;
Pred. No. 1.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                     /organism="Mus sp."
/clone="pMALP-mBC"
1. .324
                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vector_class = cosmid, Lorist 6
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14-APR-2000

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Submitted (05-JUN-1997) to the DDBJ/EMBL/GenBank databases. Hidekatsu Yoshioka, Okayama University Medical School, Molecular Biology and Biochemistry; 2-5-1 Shikata-cho, Okayama, Okayama 700, Japan (E-mail.mbb@ccews.cc.okayama-u.ac.jp, Tel:086-235-7128, Fax:086-222-7768)
                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                   Khaleduzzaman,M., Sumiyoshi,H., Ueki,Y., Inoguchi,K., Ninomiya,Y. and Yoshioka,H. Structure of the human type XIX collagen (COL19A1) gene, which suggests it has arisen from an ancestor gene of the FACIT family Genomics 45 (2), 304-312 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13.2; DB 85; Length 84; Pred. No. 2e+03; 2; Mismatches 1; Indels (
                                      ABOO468S29 84 bp DNA PRI 1
Human gene for Type XIX collagen al chain, exon 29.
ABOO4603
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/organism="Homo sapiens"
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/clone="MKG34"
                                                                                                                          Homo sapiens DNA, clone:MKG34.
Homo sapiens
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                                                                            ABO04603.1 GI:2598694
Type XIX collagen al chain.
29 of 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.0%;
80.0%;
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human STS WI-6896.
G06299
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Yoshioka, H.
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                                 AF018838 Echinomet
G36845. SHGC 60507
X56574 Mouse RAR-b
AJ276515 Mus muscu
AJ276515 Mus muscu
E09856 CDNA encodi
E11370 CDNA encodi
AF305546 Aspergill
AC057116 Giardia i
E11423 DNA encodin
M7325 MXXCCOCCUS
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AZ076870 Mus muscu
AX068319 Sequence
AX060391 Sequence
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S70577 RAR beta 1/
AJ276514 Mus muscu
U52115 Callithrix
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AJ276871 Mus muscu
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X14605 Bos taurus
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AL400931 T7 end of
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AL432214 T7 end of
AL422933 T3 end of
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AF334165 Mycobacte
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            L22859 Saimiri sci
AF221064 Meriones
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I49083 Sequence 6
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide"
8 c 10 g 2 t
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Pred. No. 2.2e+03;
2; Mismatches 1;
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Ret ligand 5 (ret15) from human and mouse Patent: WO 0116169-A 10 08-MAR-2001;
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                                                                       MMU276872
MMU276515
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AX090389
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CNS07740
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CNSO6ZY7
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Best Local Similarity 80.0
Matches 12; Conservative
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Whitehead Institute/MIT Center for Genome Research; Physically 19-0CT-1995 STS sequence; primer; sequence tagged site. human STSs derived from sequences in dbEST and the Unigene Whitehead Institute/MIT Center for Genome Research Whitehead Institute for Biomedical Research

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	AX090397 Sequence	AB004603 Human gen	G06299 human STS W	E11372 cDNA encodi	Z71056 D. melanoga	X56569 Mouse RAR-b	AR064381 Sequence	T41335 Segmence 6
QI	AX090397	AB00468S29	1 G06299	E11372	DM128B5S	MMRARB1	AR064381	141335
DB	10	85	54	45	54	94	6	10
Query Match Length DB ID	26	84	310	324	325	360	396	396
Query Match	88.0	88.0	88.0	88.0	88.0	88.0	88.0	88.0
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ssult No.	1	7	m	4	S	9	7	80

us-09-532-263-9.rng

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Polynucleotide library used to determine cancerous states of mammalian
                                                   cancer cell line polynucleotide sequence SEQ ID NO:466
                                                                                                                        breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                       colon cancer; tumour; diagnosis; gene expression product;
                                                                                                           detection; cancerous state; metastasis; identification;
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                  (first entry)
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Lamson G, Drmanac R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lamson G, Drmanac R,
Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
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                                                                                                                                                                               Homo sapiens
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                  19-MAY-2000
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15-MAY-1998;
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27-OCT-1998;
                                                      Human colon
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                                                                                         Human:
                                                                                                           probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cells
   The present invention describes isolated polynuclectides (PN) comprising a sequence selected from one of 835 nuclectide sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences producing an Expectation (E) value of 0.01 or less compared to the 835 sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the 835 sequences that are degenerately equivalent or allelic to the 835 sequences. The polynuclectides are used to modify the activity of a polypeptide involved in a polysaccharide biosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pathway in the plant. They are especially used to modulate or alter the polysaccharide content, composition or structure of the plant. AAB16268 to AAB16340 are proteins encoded by some of the polynucleotide sequence
                                                                                                                                                                                                                                                               Eucalyptus grandis; pinus radiata; Monterey pine; modification; plant cell wall; polysaccharide; polysaccharide biosynthetic pathway; transgenic plant; ds.
                                                                                                                                                                                                                              Eucalyptus grandis alpha-glucosidase DNA sequence SEQ ID NO:197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New genes encoding proteins involved in a plant polysaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant
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Pred. No. 5.2e+02;
2; Mismatches 1; Indels 0.
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(FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 126; 301pp; English.
                                                                                                                      AAA67196 standard; DNA; 298 BP.
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99US-0148426
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                    184 ACTCCAAGGACTCCA 170
1 RCTCCANGGRCTCCA 15
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Matches 12; Conserv
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Labat I;

J, Innis MA, García PD, Sudduth-Klinger, Randazzo F, Kennedy GC, Pot D, Kašsam A; Crkvenjakov R, Dickson M, Drmanac S, Lab García V, Jones LW, Stache-Crain B;

Escobedo J,

98US-0085426. 98US-0085537. 98US-0085696. 98US-0105234.

99WO-US10602

Sudduth-Klinger J;

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AAA00010 to AAA02716 represent polynucleotides isolated from CDNA libraries constructed from human colon cancer cell lines. The present libraries constructed from human colon cancer cell lines. The present denoted as method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides can be used in a method for detecting differentially expressed genes correlated with a cancerous state of mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of disparents of the cell from the cell 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor egative breast cancer, lung cancer, and colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 5.2e+02;
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80.0%;
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248 ACTCCACGGGCTCCA 234
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Best Local Similarity
Matches 12; Conserv
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Gaps

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Conservative

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1 RCTCCANGGRCTCCA 15

ò q AAA00475 standard; cDNA; 300 BP.

AAA00475, RESULT

AAA00475

polypeptide, chimeric proteins comprising Zcytor4 polypeptide and an affinity tag, and antibodies that specifically bind Zcytor4. Zcytor4 may play a role in intracellular adhesion and in the regulation or development of haematopoietic cells.

55 G; 51 T; 8 other;

Sequence 204 BP; 45 A; 45 C;

22222X8

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acute renal failure, acute nephritis, chronic renal failure, nephrotic syndrome, renal tubule defects, kidney transplants, toxic injury, hypoxic injury and trauma. The compounds are also useful for treating conditions such as neural degeneration where neural growth and regeneration according to the standard of standard desirable, e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, Tourette's syndrome, amyotrophic lateral sclerosis, as well as motor neuron disease, demyelinating disease, bacterial diseases, viral diseases, and prion diseases including Greutzfeldt Jakob disease. The compounds are also useful for treating disorders due to damage to neural tissue caused by neoplastic impingement, trauma or cerebrovascular events such as hemorrhage or emboli, and neural disorders such as mental retardation, autism, fetal alcohol syndrome, Down's syndrome and cerebral palsy. The present sequence represents an atisense oligo KD2-819 used in the characterisation of genomic clones for RetL5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the nucleotide sequence of an expressed sequence tag identified during the cloning of human cytokine receptor Zcytor4 cDNA (see AAV5596B). A cDNA containing 110 bp was obtained from human kidney cDNA library. The DNA was transfected into Escherichia coli strain DH10b and the plasmid was designated PSL690°. This has been used to generate probes to examine expression of Zcytor4. The invention provides Zcytor4 polynucleotides (see AAV5596B) and polynucleotides (see AAW80754-56), expression vectors, eukaryotic host cells which express Zcytor4
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Pred. No. 5.1e+02;
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80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
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Whitmore T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         novel human cytokine receptor Zcytor4 cDNA. It was generated by PCR amplification (see AAV55972 and AAV55972) of a human foetal kidney CDNA library. The invention provides human and mouse cytokine receptor Zcytor4 polynuclectides (see AAV55968-69) and polypeptides (see AAW80754-57), expression vectors, eukaryotic host cells which express Zcytor4, chimeric proteins comprising a Zcytor4 polypeptide and an affinity tag, and antibodies that specifically bind Zcytor4. Zcytor4 may play a role in intracellular adhesion and in the regulation or development of haematopoietic cells.
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human and mouse cytokine receptors, DNA and antibodies - also chimeric proteins, useful for promoting cell adhesion and diagnosing Burkitt's lymphoma and leukaemia
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   Length 204;
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                                Indels
                                                                                                                                                                                                                                                                                    Cytokine receptor; Zcytor4; human; cell proliferation; cell differentiation; cell adhesion; Burkitt's lymphoma; leukaemia; diagnosis; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pownder TA;
Score 13.2; DB 19;
Pred. No. 5.2e+02;
2; Mismatches 1;
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                                                                                                                                                                                                                                                           Human cytokine receptor Zcytor4 DNA probe.
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   88.0%;
80.0%;
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                                                                                                                                                                                                                             (first entry)
Query Match 88.0
Best Local Similarity 80.0
Matches 12; Conservative
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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Example 1; Page 45; 176pp; Japanese.
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                                                                                                                                                                         haemopoietin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AKS29238 ESS39300 and AAX290816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosts of blood formation disorders. Compounds identified
                                                                                                                                                                                                                                         binding to the proteins are used for the treatment of such disorders.
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                     Hemopoletin receptor protein family NR8 used for diagnosis of blood formation disorders -
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                                                                                                                                                                                                                                                                                      Length 15;
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                                                                                                                                                                                                                                                                                      Score 13.2; DB 21;
Pred. No. 5.1e+02;
                                                              (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
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                                                                                                                                                                                                                                                          Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 other;
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80.0%;
                  99WO-JP03351
                                   98JP-0214720
98JP-0297409
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ID AA290922 standard; DNA; 15
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                                                                                                                                                                                                                                                                                                       12; Conservative
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15 GCTCCAAGGGCTCCA 1
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                                                                                                 WPI; 2000-116933/10.
                                                                                 Maeda M;
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Best Local Similarity
Matches 12; Conserv
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                  23-JUN-1999;
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                                   24 - JUN-1998;
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29-DEC-1999
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                                                                                 Nomura H,
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The invention relates to the isolation of sequences encoding human haemopoietin receptor protein family NRB genes. The NRB family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences sequences sequences and AASS92488-593800 and AASS90816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NRB family proteins are used for the diagnosts of blood formation disorders. Compounds identified
                                                                                                                                                                                                                                                                                                                                                                    as binding to the proteins are used for the treatment of such disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ret ligand 5; RetL5; autophosphorylation; tumour; renal; nephrotropic; Alzhaimer's disease; Parkhason's disease; Huntington's disease; mouse; vulnerary; nootropic; anti-HTV; neuroprotective; antibacterial; ss; cerebroprotective; hemostatic; antiinflammatory; antiviral; neuroleptic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel Ret ligand polypeptide useful for suppressing growth of a tumor cell that expresses Ret and for modulating Ret signal transduction involving a cell expressing Ret polypeptide or Ret ligand polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense oligo KD2-819 for RetL5 genomic clones characterisation.
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80.0%; Pred. No. 5.1e+02;
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Matches 12; Conservative
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15 GCTCCAGGGACTCCA 1
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AAZ90885 standard; DNA; 15
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     AAZ90885/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to the isolation of sequences encoding human haemopoietin receptor protein family NR8 genes. The NR8 family sequences were initially prearched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAAS9288-259300 and AAS90816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
                                                                                                                                 Gaps
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                                                                                                 Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                          Haemopoietin receptor family; NR8; antibody; diagnosis;
blood formation disorder; fusion protein; probe; ss.
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80.0%; Pred. No. 5.1e+02;
                                                                                              Score 13.2; DB 21;
Pred. No. 5.1e+02;
2; Mismatches 1;
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                                                Sequence 15 BP; 2 A; 3 C; 6 G; 4 T; 0 other;
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                                                                                                                                                                                                                                                                           AAZ90863 standard; DNA; 15 BP.
                                                                                                 88.0%;
80.0%;
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98JP-0297409
                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                          Human NR8 gene probe #91
                                                                                                                                                               1 RCTCCANGGRCTCCA 15
                                                                                                                                                                                  15 GCTCCAAGGACTCCA 1
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                                                                                               Query Match
Best Local Similarity
Matches 12; Conserv
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Best Local Similarity
Matches 12; Conserv
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haemopoletin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid sequence Trp-Ser. The sequences AAZ59258-259300 and AA290816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the isolation of sequences encoding human
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Pred. No. 5.1e+02;
2; Mismatches 1;
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80.0%;
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98JP-0297409
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                                                                                    Human NR8 gene probe #113.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maeda M;
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Best Local Similarity
Matches 12; Conserv
                                          24-MAY-2000
                                                                                                                                                                                            Homo sapiens
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19-OCT-1998;
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AAZ90885;
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The invention relates to the isolation of sequences encoding human haemopoletin receptor protein family NRB genes. The NRB family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAX59258-559300 and AAX90816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NRB family proteins are used for the diagnosis of blood formation disorders. Compounds identified
                                                                                                                                                                                                                                                                                                                                                          as binding to the proteins are used for the treatment of such disorders.
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                                                                                   Hemopoletin receptor protein family NR8 used for diagnosis of blood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.0%; Score 13.2; DB 21; 80.0%; Pred. No. 5.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                              Example 1; Page 41; 176pp; Japanese.
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98JP-0297409
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Matches 12; Conservative
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15 GCTCCAGGGACTCCA 1
                                           WPI; 2000-116933/10.
                                                                                                         formation disorders
    Nomura H, Maeda M;
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19-OCT-1998;
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Haemopoietin receptor family; NRB; antibody; diagnosis;
blood formation disorder; fusion protein; probe; ss.
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Pred. No. 5.1e+02;
                                                                                                                                                                                                                                                                                         (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
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98JP-0297409
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15 GCTCCAGGGACTCCA 1
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19-OCT-1998;
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15 ACTCCATGGACTCCA'1
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                                                                                                                                                                                AAZ90833;
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ID AAZ908
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                               5 Degenerate hybridisation probes (AAT17870-74) are based on a conserved motif (AAR92812) found in haemopoietin receptors. The probes are used in the identification and/or cloning of genes coding for novel haemopoietin receptors, e.g. the murine interleukin-11 (IL-11) receptor alpha chain gene (AAT17868). Such receptors are defined by their ability to hybridise to the probes under medium stringency conditions.
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                                                                                                                                                                                                                                    Length 15;
                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                88.0%; Score 13.2; DB 17; 100.0%; Pred. No. 5.1e+02;
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                                                                                                                                                                            Sequence 15 BP; 2 A; 6 C; 2 G; 2 T; 3 other;
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Claim 12; Page 52; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ59273 standard; DNA; 15 BP.
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98JP-0297409
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Best Local Similarity
Matches 12; Conserv
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The invention relates to the isolation of sequences encoding human haemopoietin receptor protein family NR8 genes. The NR8 family sequences were initially presched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAAZ5928-259300 and AAZ90816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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BP.
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AAZ90833 standard; DNA; 15
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Scoring table:

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Haemopoletin; interleukin-11; IL-11; receptor; agonist; antagonist; therapy; diagnosis; probe; hybridisation; ss.
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                                                                               AAQ84638
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05-SEP-1994;
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Copyright (c) 1993 - 2000 Comp
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    nucleic search, using sw model

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D45552 235 bp mRNA EST 20-FEB-1995 HUMGS02739 Human adult lung 3' directed MboI cDNA Homo sapiens cDNA 3', mRNA sequence. D45552 GI:662506
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

( Dases 1 to 235)

Itoh,K., Okubo,K., Yosii,J., Yokouchi,H. and Matsubara,K.

An expression profile of active genes in human lung

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 1; Indels
                                                                                                                                                                                                                                                                                                                                                                  Contact: Kohichi Itoh
Institute for Molecular and Cellular Biology
Osaka University
3-1, Yamadaoka, Sulta, Osaka, 565, Japan
Tel: 06-877-5111 x3910
Fax: 06-877-1922.
 Mismatches
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Job time: 24140 sec
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Best Local Similarity 80.0
Matches 12; Conservative
Conservative
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66 GCTCCAGGGACTCCA 52
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/note="Organ: ovary; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI" 66 g 60 t
 /organism="Rattus sp."
/db_xref="ATCC (inhost):2040521"
/db_xref="taxon:10118"
/clone="ROVCI69"
                                                                                                                                                                                                                                                                                                                                                                                             AA587324.1 GI:2398138
                                                                                                                                                                    88.0%;
80.0%;
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                                                                                                                                                                    Query Match 88.0
Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                             :||||| ||:|||||
216 GCTCCAGGGACTCCA 202
                                                                                                                                                                                                                            1 RCTCCANGGRCTCCA 15
                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
AA587324
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                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                             human.
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ORGANISM
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AA587324/c
LOCUS
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                                                                                                        BASE COUNT
ORIGIN
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI234857 232 bp mRNA EST 31-JAN-1999
EST231419 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
ROVC169 3' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                         3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                                                                                                                     /clone_lib="RIKEN full-length enriched, 11 days pregnant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 232)
Lee.N.H., Gloddek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
visit our web site (http://genome.rtc.riken.go.jp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene Index
Unpublished (1998)
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seg primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                 /tissue_type="ovary and uterus"
/dev_stage="11 days pregnant, adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 13.2; DB 28;
Pred. No. 5.5e+03;
2; Mismatches 1;
                                                                                                                                     adult female ovary and uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 t
                                                           /organism="Mus musculus"
                                                                                         /db_xref="taxon:10090"
                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                        /clone="5033406C17
                                                                         /strain="C57BL/6J
                                                                                                                                                   /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AI234857.1 GI:3828363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.0%;
80.0%;
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Best Local Similarity 80.0'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BamHI.
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 Please further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI234857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus.
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AI234857/c
LOCUS
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ORIGIN
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KEYWORDS
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                               FEATURES
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/organism="Homo sapiens"
//organism="Homo sapiens"
//db_xref="taxon:9606"
//clone="INAGE:1090008"
//clone="INAGE:1090008"
//clone="INAGE:1090008"
//clone="INAGE:000 tumor RER+"
//lab_host="Duple="Colon tumor Nector: pT7T3D-Pac (Pharmacia) with a modified polylinker: 1st strand cDNA was prepared from RER+ Colon tumor, and was then primed with a Not I olygo(dT) primer. Double-stranded cDNA was ligated to colygo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3
vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (Soares4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NGI-CGAP clone distribution information on be found through the I.M.A.G.E. Consortlum/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 54 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 153.

Location/Qualifiers
                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 233)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                              AA587324 233 bp mRNA EST 26-SEP-1997 nn78e01.s1 NCI_CGAP_CO9 Homo sapiens cDNA clone IMAGE:1090008 3',
                                                                       Gaps
                                                                    ö
   Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 233;
                                                                    Indels
Score 13.2; DB 17;
Pred. No. 5.5e+03;
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Pred. No. 5.5e+03;
                                                             2; Mismatches
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Best Local Similarity
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Gaps

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VERSION

REFERENCE AUTHORS

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Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV288298 230 bp mRNA EST 09-NOV-1999 AV288298 RIKEN full-length enriched, 11 days pregnant adult female ovary and uterus Mus musculus cDNA clone 5033406C17, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
Sasaki,N., Izawa,M., watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Institute of Physical and Chemical Research (RIKEN), Genomic
                                                                                                                                                                                                                                                                                                                                                                                                            88.0%; Score 13.2; DB 28; Length 227; 80.0%; Pred. No. 5.5e+03; Live 2; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV288298.1 GI:6298802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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29 ACTCCAAGGACTCCA 15
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                              71
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DEFINITION
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L Unpublished (1999)

Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455.3460 (1998) Inch.M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Yomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y., and Hayashizaki,Y. Automated flitration-based high-throughput plasmid preparation Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                  AV282369 227 bp mRNA EST 08-NOV-1999
AV282369 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4933429K08 3' similar to AB029026 Homo sapiens MNARA for KIAA1103 protein, mRNA sequence.
AV282369.1 GI:6275118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-resettc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/dev_stage="adult"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Institute of Physical and Chemical Research (RIKEN), Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4933429K08"
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                          Sciences Center
                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
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JOURNAL
COMMENT
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FEATURES

us-09-532-263-9.rst

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Gaps

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24-FEB-2000

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Tel: 217 333 5998
Fax: 217 244 5617
Fex: 217 244 5617
Fex: 217 244 5617
Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimml 9:
Cross_match from Washington University Genome Center PHRAP suite.
Sequences submitted are vector free and at least 200 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bos.
1 (bases 1 to 226)
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Lewin, H. A. W. M. Keck Center for Comparative and Functional Genomics W. M. Keck Center for Comparative and Functional Genomics of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL 61801, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="female"
//lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP230010A20B6 Soares normalized bovine placenta Bos taurus cDNA clone BP230010A20B6 5', mRNA sequence. AW462741. GI:7032909
                                                                                                                                                     Score 13.2; DB 148; Length 221;
Pred. No. 5.5e+03;
2; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13.2; DB 116; Length 226;
Pred. No. 5.5e+03;
2; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares normalized bovine placenta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORWARD: TAATACCACTATAGGG
BACKWARD: ATTAACCTCACTAAAG
Insert Length: 226 Std Error: 0.00
Plate: BP330010A20 row: B column: 6
Seq primer: AGCGGATAACAATTTCACACAGGA
High quality sequence stop: 226.
low stringency conditions.
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/clone="BP230010A20B6"
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Matches 12; Conservative
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'Organism='Homo sapiens"

'Abrace='taxon:9606"

'Clone_lib="400047"

'dev.stage="Adult"

'note='vorgan: uterus_tumor; Vector: pucl8; Site_l: Smal;

Site_2: Smal; A mini-library was made by cloning products

Gerived from ORESTES POR (U.S. Letters Patent application

No. 196, 716 - Ludwig Institute for Cancer Research)

Profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under
                      Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 211)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagal,M.A., da Silvay,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunsteain,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0&t2=MR0-UT0047-
080900-201-d07&t3=2000-09-08&t4=1)
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MR0-UT0047-080900-201-d07 UT0047 Homo sapiens CDNA, mRNA sequence.
BF380015
GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTVN 3'], cDNA was
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Laboratory of Gancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shorgun sequencing of the human transcriptome with ORF expressed
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High quality sequence start: 56
High quality sequence stop: 219
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/dev_stage="11 weeks old"
/dev_stage="11 weeks old"
/dev_stage="11 weeks old"
/dab_bost="Sols" (kanamycin resistant)"
/note="Organ: skin; vector: pBluescript Sk-; Site_1: EcoRI
/site_2: XhoI; Cloned unidirectionally. Primer: Oligo
/dr Whole skin from II week old CS7BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAATTCGGCACGAG 3'-3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTTT" 3'"
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Marrah., Hillier, Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thelsing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                    ms24a10.rl Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:607866 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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mRNA and cDNA amplification were performed under low stringency conditions." 46 c -49\ g -48\ t
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Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
                                                                                                                            Score 13.2; DB 120; Length 198;
Pred. No. 5.4e+03;
2; Mismatches 1; Indels 0;
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/clone_lib="Stratagene mouse skin (#937313)"
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High quality sequence stop: 183.
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/strain="C57BL/6"
/db_xref="taxon:10090"
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The WashU-HHMI Mouse EST Project
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39 c
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Konno, H., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukuda, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, M., Kai, M., Kojima, Y., Koya, S., Kusakabe, M., Kojima, Y., Koya, S., Kusakabe, M., Saito, H., Sano, M., Sato, K., Shibata, Y., Shigman, T., Shigman, T., Sogabe, Y., Shigman, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Sano, M., Tominaga, M., Tsunoda, Y., Suzuki, H., Matanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Yokota, T., Yoshiki, A., Yokota, T., Yasunishi, M., Tamamatsu, M., and Hayashizaki, Y., Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Automated filtration based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
AV340647 202 bp mRNA EST . 11-NOV-1999
V3434647 RIKEN full-length enriched, adult male olfactory bulb Mus
musculus CDNA clone 6430516D09 3', mRNA sequence.
AV340647
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-resettc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
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                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 202)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
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Please visit our web site (http://genome.rtc.riken.go.jp) for
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Abb_xref="texon:10090"
/clone="6436516009"
/clone_lib="RIKEN full-length enriched; adult male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="olfactory brain"
/dev_stage="adult"
/lab_host="DH10B"
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Query Match
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Inpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: gaspbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Email: gaspbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies of the CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: NGI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Www-bio.lll.gov/bbrpy/image/image.html
Insert Length: 1894
Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 133.
                                                                                                                                                                                                                                                            rel: 81-298-36-9145
Fax: 81-298-36-9145
Exa: 81-298-36-9108
Fax: 81-298-36-9108
Fax: 81-298-36-9108
Thermostabilization and thermoactivation of thermolabile enzymes by trehablose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998)) further details.
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Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Yateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
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1 (basea 1 to 18)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="8510207Nn04"
/clone="1b="Mus musculus C57BL/6J 10-day embryo"
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                                                                                                                                                                                                                                        3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="10-day embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
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A1933508
A1933508.1 GI:5672245
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80.0%;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 198)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV4-UM0094-280 300-152-aOl&t3=2000-03-28&t4=1) Seq primer: puc 18 forward High quality sequence stop: 198.
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/note="Organ: uterus; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES FCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
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                                                                                                                                                                                                                                                                                           /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW804893 - 198 bp mRNA EST 16-MAY-2000
0V4 UM0094-280300-152-a01 UM0094 Homo saplens CDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                           /clone_lib="NCI_CGAP_Ut2"
/tlssue_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 13.2; DB 103; Length 187;
Pred. No. 5.4e+03;
2; Mismatches 1; Indels 0;
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/db_xref="taxon:9606"
/clone_lib="UM0094"
                                                                /organism~"Homo sapiens"
                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:2441698"
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
Location/Qualifiers
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55 GCTCCAGGGACTCCA 41
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male adipose"
/sex="male"
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58 GCTCCAGGGGCTCCA 44
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (basea 1 to 170)
S Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T., Carninci,P., Hanagaki,T., Hayatsu,N., Hiraoka,T., Hirozane,T., Hodoyama,Y., Imotani,K., Ishi,Y., Itoh,M., Izawa,M., Kawai,J., Kojima,Y., Konno,H., Kusakabe,M., Matsuyama,T., Miyazaki,A., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Sato,K., Shibata,K., Shibata,X., Shinagawa,A., Shiraki,T., Soapbe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Tanaka,T., Toya,T., Watahiki,A., Suzuki,H., Tagawa,A., Takahashi,F., Tanaka,T., Toya,T., Wasunishi,A., Yasunishi,A., Yasunishi,A., Yoshiki,A., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                               CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-GCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 632 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 107.
Location/Qualifiers
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The Institute of Physical and Chemical Research (RIKEN), Genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                                                                                                                                                  /clone="IMAGE:2011202"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="q1ioblastoma (pooled)"
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Pred. No. 5.3e+03;
2; Mismatches 1;
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/organism="Homo sapiens"
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Contact: Yoshihide Hayashizaki
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URL:http://genome.rtc.riken.go.jp/
Carninci.P., Nishiyama.Y., Westover.A., Itoh,M., Nagaoka,S., Sasaki.N., Okazaki.Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length DDN. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration based high-throughput plasmid preparation system. Genome. Res. 9 (5), 463-470 (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 182)
Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Site_1: Sall; Site_2: BamHI: cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
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High-efficiency full-length cDNA-cloning. Methods Enzymol. 303,
19-44 (1999)
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Pred. No. 5.4e+03;
2; Mismatches 1; Indels 0;
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Schellenberg, K. Theising, B., Waterston, R. The WashU-HHMI Unpublished (19 Contact: Marra WashU-HHMI Mous WashU-HHMI Mous Fax: 314 286 18 Fax: 314 28 Fax																								/clone /cell /lab_ /lab_ was pv was pv was pv					rapidi charac			atch cal Similarity E 12; Conservati		RCTCCAN :IIIII GCTCCAT		A1371456  gy06c0.x1 NCL mRNA sequence. A1371456 A1371456.1 GI: EST. Home sapiens Euthe Mammalia; Euthe 1 (bases 1 to NCI/NINDS-CGAP NATIONAL			Disorders and (CGAP/BTGAP), 1	Disorders and S (CGAP/BTGAP), T Unpublished (19 Contact: Robert Email: Cgapbs-1 Tissue Procuren		
TITLE JOURNAL	COMMENT						FEATURES	source									BASE COUNT ORIGIN	:	Query Match Best Local (		48		RESULT 2 A1371456/C LOCUS DEFINITION	ACCESSION	KEYWORDS	ORGANISM	REFERENCE AUTHORS		JOURNAL													
Description	AA644792 vs82d07.r AI371456 qy06c02.x	BB593914 BB593914 AV118281 AV118281	A1933508 wm74e06.x AW804893 OV4-UM009	AA163051 ms24a10.r AV340647 AV340647	BF380015 MR0-UT004	AW462/41 BP230010A AV282369 AV282369	AV288298 AV288298 AI234857 EST231419	AA587324 nn78e01.s D45552 HUMGS02739	AAO89075 mo63a01.r T03328 IB1253 Infa	C12571 C12571 Yuji H32365 EST107377 R	AII85438 qe53d09.x BBI86104 BBI80104	AA653297 A96506.s AA63297 A96506.s	AA340930 ESCU4D122 II AA340930 EST466241	BF/14535 MADULEUI. BB313515 BB313512 AT547460 MT-P-C3-S	AA494436 ne28644.s AA66643 vw386f02 x	BF228467 BP250008B BB461437 BB461437	BE631643 uu63a05.y AA288582 mp15905.r	BF290833 EST455424	AZ227737 RPCI-23-8 H34301 EST111113 R F01363 HEDDAS876 H	BF363285 CM2-NN011 BF010839 NXCI_095	AA963063 UI-R-EI-f BF931642 IL2-NT020	AA822320 vw36f02.r AI465630 vw36f02.v	•		EST 28-OCT-1997 RB5 Mus musculus cDNA clone	POINTIVE DMAN); gb:X70764 M.musculus GC (MOISE); mRNA sequence			; Vertebrata; Euteleostomi; athi; Muridae; Murinae; Mus.	Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Lacy,M., Le,M., Martin,J., Morris,M.,												
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% Query Score Match	13.2	13.2 13.2	13.2	13.2	13.2	13.2	13.2		13.2	13.2	13.2	13.5	13.2	13.5	13.2	13.2	13.5	13.2	13.2 88.0	13.2		13.2		RESULT 1	NO	SERINE/THE	ACCESSION AA644792 VERSION AA644792.1 KEYWORDS EST.	ΜS		AUTHORS Marra, M.,												
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-rêmail.nih.gov
ement: David N. Louls, M.D., Myrna R. Rosenfeld M.D.,
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neria; Primates; Catarrhini; Hominidae; Homo.
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available royalty-free through LLNL ; contact the
ium (info@image.llnl.gov) for further information.
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Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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[ bases 1 to 1290]
Pfeffer, P. L., Gerster, T., Lun, K., Brand, M. and Busslinger, M. Characterization of three novel members of the zebrafish Pax2/5/8 family; dependency of Pax5 and Pax8 expression on the Pax2.1 (noi)
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Direct Submission
Submitted (19-30W-1998) Institute of Molecular Pathology, Dr.
Bohr-Gasse 7, Vienna A-1030, Austria
Location/Qualifiers
1. 1290
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/db_xref="taxon:7955"
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/rpt_family="Alu-Jo"
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a 280 c 329 g
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QEVSPEVNSLSPSPHIISGSAFLDLSAISSPSSAPVASSCGSAHLSHGFSSFSHHAPV
HGGPSSPSLAAGREVASSMLFGYPRHIPTAGTGFSSSTIAGMVSAPEVTGGSYSHPAY
BASE COUNT 282 a 427 c 353 g 228 t
ORIGIN

Query Match

Query Match

Best Local Similarity 80.0%; Score 13.8; DB 8; Length 1290;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCTCCAYTTRCTCCA 15

QY 1 RCTCCAYTTRCTCCA 15

Search completed: August 29, 2001, 19:52:03
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mat_peptide
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                                                                                                                                                   Direct Submission
Submitted (12-MAY-1998) Biochemistry, Univ. of Texas Health Science
Center at San Antonio, 7703 Floyd Curl Dr., San Antonio, TX 78284,
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Direct Submission

Direct Gubmission

Direct (04-DEC-1992) to the DDBJ/EMBL/GenBank databases.

Tadatsugu Taniguchi, Osaka University, Institute for Mol. and Cell.

Biology; Suita-shi, Osaka 565, Japan (Tel:06-877-5289, Fax:06-878-9846)
                                                                Members of the Mouse retrovirus-related repetitive sequence MuERVC recovered from C57BL/6J and SPRET/Ei
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (strain:C57BL16) spleen cDNA to mRNA, clone_lib:mouse spleen cell cDNA.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1063)
Hardies,S.C.

    >1063
/note="similar to the gag-pol of Moloney Murine Leukemia
virus"

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 1165)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kobayashi,N., Nakagawa,S., Minami,Y., Taniguchi,T. and Kono,T. Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IL-2 receptor; cytokine receptor family; gammachain; mouse IL-2R
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                                                                                                                                                                                                                Location/Qualifiers
1. 1063
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/clone="M8"
                                                                                                                                                                                                                                                                                                                                                                                                               μ
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Tadatsugu Taniguchi
Institute for Molecular and
Cellular Biology, Osaka University
                                                                                                                                                                                                                                                                                                                                                                                                               223
                                                                                                                                                                                                                                                                                                                                                                          /rpt_type=dispersed
/rpt_family="MuERVC"
196 c 297 g
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Location/Qualifiers
1. .1165
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93366191
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80.0%;
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Hardies, S.C.
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Matches 12; Conservative
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79 ACTCCATTTGCTCCA 65
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LIFVYGWLERRPPIPIPINLEDILYTEYGCNPSAWSGVSKGLTESLQPDYSERFCHVSE
IPPRGGALGEGPGGSPCSLHSPYWPPPCYSLKPEA"
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Homo sapiens partial IL-12RB1 gene for IL-12 receptor betal chain,
exons 6-7.
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Submitted (20-SEP-2000) Abdelhak S., Immunology, Institut Pasteur
de.Tunis, BP74 13, Place Pasteur, Tunis, 1002, TUNISIA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Elloumi-Zghal,H., Abdelhak,S. and Dellagi,K. Genomic structure of IL12RB1 gene
Upublished
2 (bases 1 to 1187)
                                                                    /clone_lib="mouse spleen cell cDNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 13.8; DB 94;
Pred. No. 1.8e+03;
3; Mismatches 0;
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AJ297692.1 GI:10443211
IL-12 receptor betal chain; IL-12RB1 gene.
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74. 1114
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1 292 c 276 g 289 t
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8. .1117
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1. .1187
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Best Local Similarity 80.0
Matches 12; Conservative
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733 GCTCCATTTACTCCA 719
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LDNQKHVLSTYSTYGITISQEIISESKPGYGTWNLLGAQTVTLDNQQTPTVFYHFERT
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Mus musculus domesticus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="c in wild type; t in amber mutants N108 and N93"
                                   Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae;
T4-like phages.
                                                                      Tition property (1988)

Barrett, B.K. and Berget, P.B.
Laboratory methods using transposon Tn5 insertions to sequence bacteriophage T4 gene 11

BNA 8, 287-295 (1989)

B9356257

Braft entry and computer readable copy of sequence [1] kindly provided by P.B.Berget, 20-JUL-1989.

The reading frame for gpl2 is in disagreement with Selivanov et al., (Accession #X06792).
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/note="baseplate structural protein (gpl1)"
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Pred. No. 1.8e+03;
Bacteriophage T4 DNA, clone pJZ1 and pBB1.
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/protein_id="AAA32495.1"
/db_xref="G1:553024"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAA32494.1"
/db_xref="GI:215858"
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/note="gp12 protein"
/codon_start=1
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Mus musculus domesticus
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80.0%;
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                  Bacteriophage T4
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/product="ccAF1 protein"
/product="ccAF1 protein"
/protein_id="AaA87454.1"
/db_xref="G1:726134"
/translation="MASSSSGGAGGAGGASGAPEVKIHNVYMSNVEEEFARIRGEVED
YPYVAMDTEFPGVVATPLGTFRSKEDFNYQQVFCNVNMLKLIQVGFAMVNDKGELPPT
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RITWLTFSSGYDFGYLLKSITLGDLPKEESTFFWCHKTLFPTSFDIKILLRTPNCASA
KLKGGLQEVADQLDVKRQGVRHQAGSDALLTAATFFKIKKQFFGDNWNQIAPLICGHM
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Submitted (28-FEB-1995) Christopher Salvadore, Blochemistry
Department, University of New Hampshire, Main Syreet, Durham, NH
03824, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 1025)
Draper.M.P., Salvadore.C. and Denis.C.L.
Identification of a mouse protein whose homolog in Saccharomyces cerevisiae is a component of the CCR4 transcriptional regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PT4G11A 1034 bp DNA PHG 28-APR-1993
Bacteriophage T4D gene 11 encoding baseplate structural protein (gp11) complete cds, gene 10, 3' end, and gene 12, 5' end. M26253
M26253 G1:215856
baseplate structural protein; gp10 gene; gp11 gene; gp12 gene.
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Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                          Length 979;
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240 c 240 q 269 t
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/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
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Pred. No. 1.8e+03;
3; Mismatches 0;
                                                        Score 13.8; DB 14;
Pred. No. 1.8e+03;
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95311945
                                                                                               Mismatches
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80.0%;
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80.0%;
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Salvadore, C.
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Best Local Similarity 80.0
Matches 12; Conservative
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425 ACTCCATTTACTCCA 439
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Anopheles gambiae STS SP6 end of clone 02F01 of Notrebamel library
from strain PEST of Anopheles gambiae (African malaria mosquito),
sequence tagged site.
AL140569.1 GI:6998687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission

Submitted (16.FBE-2000) Genoscope - Centre National de Sequencage :

BP 191 91006 EFRT cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

- C hoases 1 to 900)

Roth,C.W. Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.

Direct Submission
                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 783)
Obata, Y.
Breast, gastric and prostate cancer associated antigens and uses therefor
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       African malaria mosquito.
Anopheles gambiae
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidea; Anopheles.
1 (bases 1 to 900)
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                                                        Length 748;
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Pred. No. 1.8e+03;
3; Mismatches 0; Indels
  3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 others
                                                                                    Indels
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                                                       Score 13.8; DB 53;
Pred. No. 1.8e+03;
3; Mismatches 0;
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LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
LOCALION/QUALITIERS
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 193 t
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Sequence 312 from Patent WO0073801.
AX053546
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
147 c 160 g 216
  9
  168
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80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
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AX053546/c
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1 (bases 1 to 979)
Richardson,J.E., Fay,M.F., Cronk,Q.C., Bowman,D. and Chase,M.W.
A phylogenetic analysis of Rhamnaceae using rbcL and trnL-F plastid
DNA sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGS; intergenic spacer; transfer RNA-Leu (UAA); transfer RNA-Phe; tRNA-Leu (UAA) gene; tRNA-Phe gene.
Reissekia smilacina.
Chloroplast Reissekia smilacina
Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rhamnaceae; Reissekia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSM390345 979 bp DNA PLN 09-NOV-2000 Reissekia smilacina chloroplast partial tRNA-Leu(UAA) and tRNA-Phegenes and intergenic spacer, IGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 979)
Richardson J.E.
Direct Submission
Submitted (28-OCT-1999) Richardson J.E., Herbarium, Royal Botanic Garden, Edinburgh, 20A Inverleith Row, Edinburgh, EH3 5LR, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                        Gaps
Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.
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                                                                                                                                                                                                                                                                                                                              Length 900;
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/db_xref="taxon:106700"
/country="Brazil"
<1. 596
/gene="tRNA-Leu(UAA)"
/product="transfer RNA-Leu(UAA)"
                                                                                                                                                                                                                                                                                                                         Score 13.8; DB 53;
Pred. No. 1.8e+03;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Reissekia smilacina"
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/gene="tRNA-Leu(UAA)"
597...945
/note="intergenic spacer, IGS"
                                                                                                          /organism="Anopheles gambiae"
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946. 979
/gene="tRNA-Phe"
184 c 169 g 287 t
                                                                                                                                                                                                                                        307
                                                                                                                                           /db_xref="texon:7165"
/clone="02F01"
/clone_llb="NotreDame1"
/note="end : SP6"
a 169 c 159 g 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="tRNA-Leu(UAA)"
547. .596
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                                                               Location/Qualifiers
1..900
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/gene="tRNA-Phe"
                                                                                                                              /strain="PEST"
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AJ390345.1 GI:9968789
                                                                                                                                                                                                                                                                                                                           92.0%;
80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
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RESULT 4 LAU72036/c LOCUS

Matches

ò q

ORIGIN

DEFINITION

ACCESSION KEYWORDS SOURCE

VERSION

ORGANISM

REFERENCE AUTHORS

TITLE

AUTHORS JOURNAL

FEATURES

JOURNAL REFERENCE

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/product="interleukin-12 receptor"
/protein_id="AAR73397.1"
/protein_id="AAR73397.1"
/bcotein_id="G1:8132793"
/translation="G2ODDDTESCLOPLEMNVAQEFQLRRRRLGSGGSSWSKWSSPVC
VPPENPPQPQVRFSVDHLGRDGRRRLTLKQQPTQLELPKGCQGPAPGAEVTYQLQLHM
LSCPCKAKATRTLPLEKMPYLSGAATWMLVISSNRFGLAQTRRGTFLLTPTQKPGVLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNSOlKVY 748 bp DNA STS 17-FEB-2000 Anopheles gambiae STS SP6 end of clone 17P09 of NotreDamel library from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)
Arredondo,J.
Direct Submission
Submitsed (24-JAN-2000) California Regional Primate Research
Center, University of California-Davis, One Shields Avenue, Davis,
CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roth, C. W., Brey, P.T., Ke, Z., Collins, F.H. and Weissenbach, J. Direct Submission
Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, Franca and an Accordance of the Accordance of From Accordance of Submission Submission of Biochem. and Biol. Molec. of Insects, Institut
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
                                                                                                                                          /organism-"Macaca mulatta"
/db_xref="taxon:9544"
/db_type="peripheral blood mononuclear cells"
<1. -3487
/gene="IL-12R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 487;
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Pred. No. 1.8e+03;
3; Mismatches 0;
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                                                                                                                                                                                                                                                                             /gene="IL-12R"
/note="membrane receptor"
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/clone="17P09"
/clone_lib="NotreDame1"
/note="end : SP6"
                                                                                                          Location/Qualifiers
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1. .748
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AL148863.1 GI:7007009
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                                                                                                                                                                                                                                                              <1. .>487
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Best Local Similarity 80.0
Matches 12; Conservative
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122 GCTCCACTTGCTCCA 108
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JOURNAL
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Petrygota: Neoptera: Endopterygota; Hymenoptera; Apocrita;
Aculeata; Formicidae; Myrmicinae; Leptothorax.

1 (bases 1 to 271)
Brachtody, Green, H.A.A. and Bourke, A.F.G.
Parentage, reproductive skew and queen turnover in a multiple-queen ant analysed with microsatellites
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Bruford,M.W., Green,H.A.A. and Bourke,A.F.G.
Direct Submission
Submitsed (19-58P-1996) Conservation Genetics Group, Institute of Zoology, Regent's Park, London NW1 4RY, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF227552 487 bp mRNA PRI 01-JUN-2000
Macaca mulatta interleukin-12 receptor (IL-12R) mRNA, partial cds.
AF227552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.

(bases 1 to 487)
                                                                                                                                                                                                                                                                                                          Leptothorax acervorum microsatellite LXA GA 1, complete sequence. 0772036
                                                                                                             Gaps
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                                                                Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 271;
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                                                                                                          Indels
                                                            Score 13.8; DB 95;
Pred. No. 1.8e+03;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Leptothorax acervorum"
/db_xref="taxon:33409"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 13.8; DB 6;
Pred. No. 1.8e+03;
3; Mismatches 0;
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/rpt_type=tandem
/rpt_unit=ag 41 t
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/note="LXA GA 1"
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80.0%;
                                                                92.0%;
80.0%;
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Matches 12; Conservative
                                                                                                        12; Conservative
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137 GCTCCAFTTACTCCA 123
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211 GCTCCACTTGCTCCA 197
                                                                                                                                                   1 RCTCCAYTTRCTCCA 15
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Macaca mulatta
                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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DEFINITION ACCESSION

LOCUS

SOURCE ORGANISM

KEYWORDS

VERSION

TITLE JOURNAL REFERENCE

REFERENCE AUTHORS

RESULT 5 AF227552/c

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BASE COUNT

ORIGIN

; 0

Gaps

; 0

us-09-532-263-10.rge

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Gorman, D.M., Itoh, N., Jenkins, N.A., Gilbert, D.A., Copeland, N.G. and
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DiSanto, J.P., Certain, S., Wilson, A., MacDonald, H.R., Avner, P.,
Fischer, A. and Ge Sahit Basile, G.
The murine interleukin-2 receptor gamma chain gene: organization, chromosomal localization and expression in the adult thymus
Eur. J. Immunol. 24 (12), 3014-3018 (1994)
                                                                                                                                                                                                                                                                                 Chromosomal localization and organization of the murine genes encoding the beta subunits (AIC2A and AIC2B) of the interleukin 3, granulocyte/macrophage colony-stimulating factor, and interleukin
                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus sp. liver BALB/c.
Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                      M95509.1 GI:191832
GM-CSF receptor B-subunit; IL-3 receptor B-subunit; IL-5 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenBank staff at the National Library of Medicine created this entry (NCBI gibbsq 161704) from the original journal article. This sequence comes from Fig. 2 and 3. Map location: X region 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  $7584455 179 bp DNA ROD 15-JUN-1995 IL-2R gamma -interleukin-2 receptor gamma chain [mice, BALB/c, liver, Genomic, 179 nt, segment 5 of 8].
$575849 GI:861551
                    LOCUS MUSAIC2B10 160 bp DNA ROD 27-APR-1993 DEFINITION MUS musculus IL-3, IL-5, and GM-CSF receptor B-subunit (AIC2B)
                                                                                                                                                          Mus musculus (strain BALB/c, sub_species domesticus) DNA.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 160;
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Pred. No. 1.8e+03;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 267, 15842-15848 (1992) 92348451
                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="BALB/c"
/sub_species="domesticus"
/db_xref="taxon:10090"
1. .160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25
                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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/organism="Mus sp."
/db_xref="taxon:10095"
a 37 c 50 g
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80.0%;
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132 GCTCCACTTGCTCCA 118
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                                                       gene, exon 10.
M95509
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                         B-subunit.
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MUSAIC2B10/c
LOCUS
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REMARK
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U86145 Influenza A
U87970 Influenza A
U31946 Influenza A
U53166 Influenza A
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AF056218 Bos tauru
AF077299 Drosophil
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Stinchcomb,D.T. and McSwiggen,J.A.
Interleukin-2 receptor gamma-chain ribozymes
Patent: US 5807743-A 809 15-SEP-1998;
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Sequence 809 from patent US 5807743.
AR039961
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TITLE
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Database

M95509 Mus musculu 877849 LL-2R gamma V72036 Leptchhorax AF227552 Macaca mu AL148863 Anopheles AX053546 Sequence AL140569 Anopheles

AR039961 Sequence

Description

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A cDNA library of PHA-activated peripheral blood mononuclear cells in vector pEF-BOS was screened for interleukin-12 (IL-12) receptor cDNAs by panning. An isolated cDNA was sequenced (AAQ83844); it encoded a 662-amino acid low affinity IL-12 receptor (AAR69632). Recombinant IL-12 receptor was expressed in COS cells, and can be used for therapeutic or diagnostic purposes.
                                                                                                                                                                                                                                                                                                                  DNA encoding a low affinity interleukin-12 receptor - used to
bind or scavenge IL-12 to cause immune suppression, e.g. to
suppress graft-vs-host reaction, allograft rejection or
inflammation, and to treat autoimmune conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2104 BP; 411 A; 624 C; 658 G; 411 T; 0 other;
                                                                                                                                                                                                                                               Chizzonite RA, Chua AO, Gubler UA, Truitt TP;
           Location/Qualifiers
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93US-0094713.
94US-0248532.
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19-JUL-1993;
31-MAY-1994;
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Search completed: August 29, 2001, 20:16:45 Job time: 7426 sec

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Query Match
92.0%; Score 13.8; DB 16; Length 2104;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 3; Mismatches 0; Indels 0;

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990S-0141287.
990S-0142154.
990S-0142055.
990S-0142930.
990S-0142920.
990S-0142977.
990S-0143624.
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99US-0151066.
99US-0151080.
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Interleukin-12 receptor: IL-12; immune suppression; immunosuppressive; graft-versus-host reaction; allograft rejection; inflammation; autoimmune disease; ds.
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               990S-0151438
990S-0151930
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990S-0154018
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99US-0160770.
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1223 ACTCCACTTGCTCCA 1209
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30 - AuG - 1999;
31 - AuG - 1999;
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Homo sapiens

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
 Arabidopsis thaliana DNA fragment SEQ ID NO: 49177.
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990S-0129845.
990S-0130077.
990S-0130449.
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99US-0137222.
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99US-0139462
                                                                       Arabidopsis thaliana.
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16 - JUN - 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diagnosis of X-linked severe combined immunodeficiency (XSCID) comprises detecting mutated IL-2R gamma gene, also vectors and transgenic animals containing the mutated gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ71977 is the DNA sequence of murine IL-2R gamma AAR59094, this was used in the development of a claimed method for the diagnosis of X-linked severe combined immunodeficiency (XSCID), in female carriers and male sufferers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 13.8; DB 15; Length 1608;
Pred. No. 2.5e+02;
3; Mismatches 0; Indels 0;
                                                                                                                                                       Murine IL2-R gamma; X-linked severe combined immunodeficiency; XSCID; interleukin; ss.
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/transl_except= pos:1015..1017, aa:His
25..82 /
/*tag= b
/note= "Putative"
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25..1134
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                                                        AAQ71977 standard; DNA; 1608 BP.
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80.0%;
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93US-0121435
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Best Local Similarity 80.0
Matches 12; Conservative
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750 GCTCCATTTACTCCA 736
891 GCTCCACTTACTCCA 877
                                                                                                                               Murine IL-2R gamma gene.
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P-PSDB; AAR59094.
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14-SEP-1993;
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PR 11-AUG-11999 990US 0148171.

PR 12-AUG-11999 990US 0148171.

PR 11-AUG-11999 990US 0148171.

PR 12-AUG-11999 990US 01481864.

PR 20-AUG-11999 990US 0149723.

PR 20-AUG-11999 990US 0149723.

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PR 21-AUG-11999 990US 0149972.

PR 22-AUG-11999 990US 014992.

PR 22-AUG-11999 990US 014992.

PR 22-AUG-11999 990US 014992.

PR 22-AUG-11999 990US 014992.

PR 21-AUG-11999 990US 011990.

PR 21-AUG-11999 990US 011990.

PR 21-AUG-11999 990US 011990.

PR 21-AUG-11999 990US 011900.

PR 21-AUG-11999 990US 01140.99.

PR 21-AUG-11999 990US 01182.29.

PR 21-AUG-11999 990US 01182.29.

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PR 21-AUG-11999 990US 01182.29.

PR 21-AUG-11999 990US 01199.

PR 21-AUG

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Gaps

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Length 1537;

Score 13.8; DB 21; Pred. No. 2.5e+02; 3; Mismatches 0;

Query Match 92.0%; Best Local Similarity 80.0%; Matches 12; Conservative 3

RCTCCAYTTRCTCCA 15 : | | | | | | | | | | | |

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99US-0134256.
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99US-0127462
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                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2000 (first entry)
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                                                                           Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                    1 RCTCCAYTTRCTCCA 15
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                                                      Query Match
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AAC36394/c
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(a) an ECORI site within a region corresponding to a 3.2 kb subfragment of the HindIII K fragment which contains both a HindIII and an ECORI site, of the SPV genome, and optionally (b) an AccI site within a region corresponding to a 3.6 kb HindIII work in a region corresponding to a 3.6 kb HindIII to BglIII subfragment of the HindIII M fragment. The recombinant SPV can be used in a vaccine for immunising an animal against SPV. The invention also provides a method for testing a content, particularly containing S-SPV-008, or is infected with a conturnally occurring wild-type pseudorabies virus. Also (I) inserted into recombinant SPV can be used in a diagnostic assay, e.g. Feline immunodeficiency virus (FIV) env and gag genes and Dirofilaria immitis made to detect heartworm caused by D. immitis respectively.
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                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic DNA SEQ ID NO:228 from WO9804684 encoding SEQ ID NO:229.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant swine pox virus – useful in vaccine for immunising animal against swine pox virus
Pred. No. 2.4e+02; .
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                                                    3; Mismatches
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1..1414
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                       80.08;
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                                                 12; Conservative
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803 GCTCCACTTACTCCA 789
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                          Best Local Similarity
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                                                                                              Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
Length 1414;
          Indels
                                                                                    Arabidopsis thaliana DNA fragment SEQ ID NO: 13639.
92.0%; Score 13.8; DB 19; 80.0%; Pred. No. 2.5e+02;
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	Length 1290;
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	DB 21;
	13.8;
	Score
S-0147260 S-0147303. S-0147303. S-01474016. S-01474016. S-01474016. S-01474017. S-01474017. S-01474017. S-01474017. S-0148171. S-0148171. S-0148171. S-0148171. S-0148171. S-0148171. S-0148171. S-0148171. S-0148171. S-0148171. S-0148171. S-0148171. S-0148171. S-0148171. S-0148171. S-0148171. S-0148171. S-0148171. S-0148171. S-0158186. S-0158186. S-0158186. S-0158186. S-0158186. S-0158186. S-0158186. S-015818. S-	162142. 92.0%;
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polynucleotides, based on which tissues they are most highly expressed (see AA224811 for described uses).
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                                                                                                         Length 1217;
                                                                                                                                         Indels
                                                    Seguence 1217 BP; 346 A; 232 C; 223 G; 416 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana DNA fragment SEQ ID NO: 58287.
                                                                                                   Score 13.8; DB 20;
Pred. No. 2.4e+02;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                 . AAC48659 standard; DNA; 1290 BP
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99US-0128234.
99US-0128714.
99US-0129845.
                                                                                                       92.0%;
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99US-0123548.
99US-0125788.
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99US-0132048
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99US-0132485
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99US-0134218
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99US-0137222
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                                                                                                 Query Match
Best Local Similarity 80.0
Matches 12; Conservative
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1076 ACTCCACTTGCTCCA 1062
                                                                                                                                                                          1 RCTCCAYTTRCTCCA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1033405-A2.
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                                                                                                                                                                                                                                                                                                                                    AAC48659;
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                                                                                                                                                                                                                                                                                   AAC48659/
                                                                                                                                                                                                            q
 22×3
                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                    This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Protein as compared to increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 95 novel genes and their fragments (nucleic acid sequences: AAZA8811-22A807; amino acid sequences AAX41308-Y41404) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 95
                                                                                                                                                                                                                                                        Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthitis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated human genes, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soppet DR;
1r DW;
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, Lafleur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen CA, Yu G, Young PE, Fel
A, Duan RD, Kyaw H, Ebner R,
                                                                                                                                                                                                                             Human secreted protein gene 26 clone HPMFP40.
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                                                                                                     AA224836/c
ID AA224836 standard; DNA; 1217 BP.
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98US-0078573.
98US-0078574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
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98US-0080312
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                                                                                                                                                                                          (first entry)
1 RCTCCAYTTRCTCCA 15
                  Wei Y, Endress GA,
Olsen HS, Shi Y, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-562050/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAY41333
                                                                                                                                                                                          02-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09947540-A1.
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10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-MAR-1999;
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01-APR-1998;
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Score 13.8; DB 21; Length 494;

Pred. No. 2.3e+02; 3; Mismatches

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diabetes, digestion disorders and wound healing disorders. The nucleic acids, antagonists or agonists of Exo proteins are useful in gene therapy. The nucleic acids are also useful for generating transgenic or knock-out animals which can be used in the
                                                                       development and screening of therapeutically useful reagents.
                                                                                                       Sequence 494 BP; 125 A; 135 C; 129 G; 101 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                      AAF22733 standard; cDNA; 783 BP.
                                                                                                                                                          92.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                             12; Conservative
                                                                                                                                                                                                                                                  1 RCTCCAYTTRCTCCA 15
                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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10-SEP-1999;
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                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Exocytosis pathway protein; Exo protein; antiparkinsonian; antidiabetic; antialergic; antiasthmatic; nootropic; neuroprotective; anticonvulsant; vulnerary; asthma; inflammation; allergy; Chediak-Higashi syndrome; CHS; Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes; digestion disorder; wound healing disorder; gene therapy; ss.
allergy and other inflammatory conditions. The ribozymes are also used to induce tolerance in a recipient to alloantigen from a donor.
                                                                                                                                            Gaps
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                                                                                                      Length 17;
                                                                                                                                        Indels
                                                                                                       DB 19;
                                                                                                    Score 13.8; DB 19;
Pred. No. 1.8e+02;
3; Mismatches 0;
                                                   Sequence 17 BP; 6 A; 1 C; 7 G; 3 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                     Mouse IL-3 receptor nucleotide sequence #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 302-303; 305pp; English.
                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                      3;
                                                                                                                                                                                                                                                                                              AAA89732 standard; cDNA; 494
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990S-0117308.
990S-0117319.
990S-0118177.
990S-0118177.
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99US-0119998.
99US-0119759.
                                                                                                    Query Match 92.0%;
Best Local Similarity 80.0%;
Matches 12; Conservative
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                                                                                                                                                                         1 RCTCCAYTTRCTCCA 15
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                                                                                                                                                                                           WPI; 2000-482908/42.
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                                                                                                                                                                                                                                                                                                                                  AAA89732;
   allergy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                condition characterised by expression of an abnormal amount of a protein,
Human gastric cancer associated antigen nucleotide sequence SEQ ID:312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                 Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 50; Page 375-376; 799pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000; 2000WO-US14749.
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haemopoietin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ55258-Z59300 and AAZ90816-Z20925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified
                                                                                                                                                                                                                                                                                                                                       as binding to the proteins are used for the treatment of such disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence invention describes ribozymes targeted to modulate the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA. AAV93889 to AAV94574 represent specifically claimed ribozymes, and AAV94575 to AAV95260 represent specifically claimed substrate sequences from the present invention. The ribozymes can be used for the treatment of, e.g. graft rejection, autoimmune disease, cancer, psoriasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain; hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer; autoimmune disease; psoriasis; allergy; inflammatory disease;
                                                                             Hemopoletin receptor protein family NR8 used for diagnosis of blood
                                                                                                                                                                                encoding human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ribozymes targeted to interleukin 2 - useful for treating e.g. cancer, autoimmune disease and allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                The invention relates to the isolation of sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse IL-2 receptor g-chain substrate position 725.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 13.8; DB 21;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                            Sequence 15. BP; 4 A; 1 C; 7 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                       Example 1; Page 45; 176pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     92.0%;
80.0%;
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Matches 12; Conservative
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                                                                                                  formation disorders
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  Maeda M;
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  Nomura H,
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Haemopoietin receptor family; NR8; antibody; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemopoletin receptor family; NRB; antibody; diagnosis; blood formation disorder; fusion protein; probe; ss.
                blood formation disorder; fusion protein; probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13.8; DB 21;
Pred. No. 1.7e+02;
3; Mismatches 0;
                                                                                                                                                                                                                                                                          CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
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80.0%;
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98JP-0297409
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98JP-0297409
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AAZ90914 standard; DNA; 15
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Best Local Similarity 80.0
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                   Maeda M;
                                                           Homo sapiens
                                                                                              WO9967290-A1
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19-OCT-1998;
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Haemopoietin receptor family; NR8; antibody; diagnosis; blood formation disorder; fusion protein; probe; ss.
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                                                                                                                                                      AAZ90874 standard; DNA; 15
                                                                                                                                                                                                                                                                  Human NR8 gene probe #102
                          1 RCTCCAYTTRCTCCA 15
                                              WPI; 2000-116933/10
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AAZ90907/c
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                                                                                                                                                                                                                                                                                     Gaps
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                                    5 Degenerate hybridisation probes (AAT17870-74) are based on a conserved motif (AAR92812) found in haemopoietin receptors. The probes are used in the identification and/or cloning of genes coding for novel haemopoietin receptors, e.g. the murine interleukin-11 (IL-11) receptor alpha chain gene (AAT17868). Such receptors are defined by their ability to hybridise to the probes under medium stringency conditions.
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                                                                                                                                                                                         Sequence 15 BP; 2 A; 6 C; 0 G; 4 T; 3 other;
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Claim 12; Page 52; 87pp; English.
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98JP-0297409
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99WO-JP03351 98JP-0214720 98JP-0297409

Maeda M;

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                                                                                                                                                                 haemopoietin receptor protein family NR8 genes. The NR8 family agequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid sequence Trp-Ser-Xaa-Trp-Ser. The sequences AKS29288-259300 and AAX290816-290925 represent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified
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Hemopoietin receptor protein family NR8 used for diagnosis of blood formation disorders - \,
                                                                                                                                         The invention relates to the isolation of sequences encoding human
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15 BP; 5 A; 0 C; 6 G; 4 T; 0 other;
                                                                                      Example 1; Page 43; 176pp; Japanese.
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15 ACTCCATTTACTCCA 1
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92.0%; Score 13.8; DB 21; 80.0%; Pred. No. 1.7e+02; tive 3; Mismatches 0;

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Query Match Best Local Similarity Matches 12; Conserv

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Human NRB gene pro
Human NRB gene pro
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31.258 Million cell updates/sec
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                                                                                                          Search time 301.32 Seconds
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Human NR8
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| SIDSB/gcgdata/geneseq_geneseq_n/NA1981 DAT:*
| SIDSB/gcgdata/geneseq_geneseq_n/NA1991 DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                       730101 seqs, 313950809 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                            August 29, 2001, 20:16:43;
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Listing first 45 summaries
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AAE22733
AAZ24836
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AAV26248
                                                                         OM nucleic - nucleic search, using sw model
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AAZ90859
AAZ90874
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15
1 RCTCCAYTTRCTCCA 15
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Arabidopsis thalia Murine IL-2R gamma Arabidopsis thalia Human interleukin-Human interleukin-Human interleukin-Human interleukin-CDNA sequence of t A. thaliana Ethyle Gravitropism stimu Murine Osteogenic Murine Osteogenic Murine DNA sequence Human Secreted prohizine DNA sequence Human LIF-R vione Human LIF-R vione Human LIF-R. Homo Human Lie-R. Homo Human leukaemia in Human propessyle WSXWS degenerate p Human propomem embrane-Human genembrane	Human secreted pro Human secreted pro Zea mays DNA fragm Candida albicans p Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia BAC containing rep Probe 9560 for hae Human TPST-1 CDNA	or; agonist; antagonist; s
AAC36394 AAC76177 AAC46177 AAC46177 AAC45332 AAAL1001 AAAL1001 AAAL29279 AAC52490 AAC57349		recept Lion; s eceptor alpha
2.0 1683 152 20 1683 152 20 20 20 20 20 20 20 20 20 20 20 20 20	0.0 436 0.0 6480 0.0 762 0.0 1485 0.0 1569 0.0 15185 0.3 3 30	first entry) (first entry) receptor probe interleukin-1 nosis; probe; 95w0-AU00578 94AU-000790; 94AU-000790; 00ERATIONS PY ancoding haem cif esp. IL-1.
5 4 4 3 2 5 4 5 5 5 6 2 6 2 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	8 8 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	AAT17874 s AAT17874; AAT17874; 21-MAY-199 daemopoiet daemopoiet cherapy; d Synthetic. 44-MAR-199 55-SEP-199 55-SEP-199 55-SEP-199 66-SEP-199 75-SEP-199 75
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hermaphrodite cDNA library. Partially normalized by
successively picking groups of clones that didn't
hybridize to previously picked clones. Vector: lambdaphage
SHLX2 (Lipshitz, D.H. et al., Gene 88:25-36 (1990)) Host:
MC1061"
                                                                                                                                         Contact: Waterston R.H.(USA) and Sulston J.E.(UK)
(USA) Dept. of Genetics or (UK)
(USA) Washington Univ. School of Medicine or (UK) MRC Laboratory of
Molecular Biology
Box 8232,4566 Scott Ave., St. Louis, MI 63110, USA, or, Hills Road
, Cambridge CB2 2QH, UK
Tel: (USA) (314)3627072 or (UK) (0223)248011
Fax: (USA) (314)3624137 or (UK) (0223)402008
Email: rw@nematode.wustl.edu or jes@mrc-lmba.cambridge.ac.uk
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1 (bases 1 to 324)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó,
,L., Durbin,R.K., Green,P., Shownkeen,R., Halloran,N., Hawkins,T., Wilson,R., Berks,M., Du,Z., Thomas,K., Thierry-Mieg,J. and Sulston

        BF936011
        324 bp
        mRNA
        EST
        22-JAN-2001

        IL2-NT0198-291200-291-B05
        NT0198
        Homo sapiens cDNA, mRNA sequence.

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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
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Pred. No. 2.4e+03;
3; Mismatches 0; Indels 0;
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20202663
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/organism="Caenorhabditis elegans"
/strain="Bristol N2"
/db_xref="taxon:6239"
/clone="cm21f10"
/clone_lib="Chris Martin sorted cDNA library"
/lab_host="MC1061"
                                                                       survey of expressed genes in Caenorhabditis elegans tture Genet. 1, 114-123 (1992)
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                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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BF936011.1 GI:12353335
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80.0%;
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Fax: +55-11-2707001
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Best Local Similarity 80.0
Matches 12; Conservative
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80 GCTCCACTTGCTCCA 66
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BF936011/c
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Nr0198"
/dev_stage="Adult"
/note="Organ: nervous_tumor; Vector: pucl8; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions.
10 thers
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=LL2&t2=LL2-NT0198-291200-291-B05&t3=2000-12-29&t4=1) Seq primer: puc 18 forward High quality sequence stop: 72.
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Matches 12; Conserv
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BASE COUNT ORIGIN

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT 12

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B75501/c

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

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Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota: Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 324)
Waterston, R., Martin, C., Craxton, M., Huynh, C., Coulson, A., Hillier
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 305)
Mahairas, G.G., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S., Traicoff, R., Abajian, C., Blanchard, A., West, A. and Hood, L.E. Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MB9352 324 bp mRNA EST 16-SEP-1992
CELLIF10 Chris Martin sorted cDNA library Caenorhabditis elegans
CDNA clone cm21f10 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                 B40700 305 bp DNA GSS 18-OCT-1997
HS-1052-A1-E09-MF.abi CIT Human Genomic Sperm Library C Homo
Sapiens genomic clone Plate=CT 774 Col=17 Row=I, DNA sequence.
B40700 GI:2544952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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/clone="plate=Cr 774 Col-17 Row=I"
/clone_lib="CIT Human Genomic Sperm Library C"
                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tagged Connectors
Unpublished (1997)
Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seatile, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackron@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 13.8; DB 256;
Pred. No. 2.4e+03;
3; Mismatches 0;
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    Pred. No. 2.4e+03; 3; Mismatches 0
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Plate: CT 774 row: I column: 17
Class: BAC ends
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Location/Qualifiers
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Best Local Similarity 80.0
Matches 12; Conservative
                      12; Conservative
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M89352/c
                        Matches
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Golden
1 Venter
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Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please context Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAce3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 291)
Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., G.,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of BAC End Sequences for Sequence-Ready Map Building Unpublished (1997)
Other GSSS: RPCIII-16K9 TP
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
712: 301 838 0200
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                     0;
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Pred. No. 2.4e+03;
3; Mismatches 0; Indels 0;
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/db_xref="GDB:7506008"
/db_xref="taxon:9606"
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Location/Qualifiers
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80.0%;
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B75501.1 GI:2771188
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150 ACTCCATTIGCTCCA 136
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Query Match

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BB585089/c
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                                                                  Manualian bullerian, Accented, Strutty Cardines, Full (Dases 1 to 272)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Etkuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, T., Kai, C., Kavai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuno, Y., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okasaki, Y., Ono, T., Owa, C., Salto, H., Sakai, C., Sato, K., Shibata, K., Shigemoto, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Toya, Y., Suguki, H., Suzuki, H., Yaugawa, A., Takahashi, F., Tominaga, N., Toya, T., Yanghi, H., Suzuki, M., Watahiki, A., Yokhi, Y., Suzuki, M., Watahiki, A., Yokhia, Y., Yamamura, T., Yamanaka, I., Yamantsu, M. and Hayashizaki, Y. Soshino, M. Muramatsu, M. and Hayashizaki, Y. Suzuki, M., Watahiki, A., Yoshiki, A., Yoshiki, A., Yoshihod Bayashizaki, Y. Contact: Yoshihde Hayashizaki Genome Exploration Research Group, Life Science Tsukuba Center, Assonne Science Ishurakan.
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URL:http://genome.rtc.riken.go.jp,
carninci.p., Nishiyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
A., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehanose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad.Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
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Automated filtration-based high-throughput plasmid preparation
System. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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/lab_host="DH10B"
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                                             Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/clone_lib="RIKEN full-length enriched, 12 days embryo
spinal cord"
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
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/db_xref="taxon:10090"
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DB 133; Length 272;

Score 13.8; DB 13. Pred. No. 2.4e+03;

92.0%; 80.0%;

Query Match Best Local Similarity

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Journal Source Center 1 Royadai, Tsukuba, Ibaraki 305-0074, Japan Tel: +81-298-36-9013

Fax: +81-298-36-9013

Fax: +81-298-36-9093

Email: genome-resertc.riken.go.jp,
URL: http://genome.rtc.riken.go.jp,
Carninci, p. Nishiyama.Y. Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.
High-efficiency full-length CDNA cloning. Methods Enzymol. 303,
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Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                           BB585089 RIKEN full-length enriched, 12 days embryo, embryonic body between diaphragm region end neck Mus musculus cDNA clone 9430004A045', mRNA sequence.
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/db_arref="taxon:10090"
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/clone=lib="RIKEN [ull-length enriched, 12 days embryo, embryonic body between diaphragm region and neck"
/tissue_type="embryonic body between diaphragm region and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 287)
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/note="Site_1: Sal1; Site_2: BamHI; cDNA library was
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1 RCTCCAYTTRCTCCA 15
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Lambda ZAP II cDNA library was constructed from mRNA extracted from etiolated leaf tissue of the rice cultivar 'IR36' and converted to pBluescript (amp resistant) as described in Causse et al. (1994) Genetics 138:1251-1274. For insert amplification, Use MI3 forward and reverse primers. Clones from this library are designated with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotta; Metazota; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 240)

1 (bases 1 to 240)

2 (M., Miyata, A. and Nishigaki, A. Expression map of the C.elegans genome
Contact: Yuji Kohara
Gene Library Lab
Mational Institute of Genetics
Mational Institute of Genetics
Tel: 81-559-81-6884
Fax: 81-559-81-6855
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                                                                                                                                                                                                                                                                                                                                                            C42038 Yuji Kohara unpublished CDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans CDNA clone yk284c9 5', mRNA sequence.
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/clone="yty34c9"
/clone="yty34c9"
hermaphrodite embryo"
/sex="hermaphrodite"
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Pred. No. 2.3e+03;
3; Mismatches 0; Indels 0:
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Pred. No. 2.3e+03;
3; Mismatches 0; Indels (
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Location/Qualifiers
1. .240
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Mus musculus

Bukarayota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

( Dases 1 to 248)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB420958 RIKEN full-length enriched, 12 days embryo spinal cord Mus musculus cDNA clone C530024L16 3', mRNA sequence.
BB420958.1 GI:9242313
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                                                                                                                                                                                                                                                                                                                                Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db.xref="taxon:10090"
/clone="IMAGE:1398826"
/clone_lib="Soares_mammary_gland_NbMMG"
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Seq primer: -28mil srev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/dev_stage="4 weeks"
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                                                                                                                                                                                                                                                                               Unpublished (1996)
Contact: Marra M/Mouse EST Project
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/organism="Mus musculus"
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Cornell University
Ithaca, NY 14853-1901, USA
Tel: 607 255 6043
Email: 507 255 6683
Email: srm4@cornell.edu
cDNA from Trice (Oryza sativa); forward sequence of RFLP probe
RZ612. Sequence determined by Nicola M. Ayres. For mapping
information, additional citations and other related information
concerning this probe, please refer to the RiceGenes database at
http://ars-genome.cornell.edu/cgi%2Dbin/WebAce/webace?db=ricegenes6
class=Marker&object=RX612.
                                                                                                                                                                                                                                                                           /clone_lib="Mouse brain, Stratagene"
/lab_host="E. coli XL1-Blue"
/note="Vector: Lambda 2AP; Site_1: EcoR I; Site_2: Xho I;
The mouse brain library (Stratagene ) was constructed by oligo-(dT) priming and directional cloning in Uni-ZAP XR phage using whole brain mRNA from a Balb C post natal 20
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/clone="Rx612"
/clone_lib="cDNA from rice"
/note="Vector: Lambda 2AP II/pBluescript; Site_1: EcoRI; A
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Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA231776 231 bp mRNA EST 15-SEP-2000 RZ612.F cDNA from rice Oryza sativa cDNA clone RZ612, mRNA sequence.
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Pred. No. 2.3e+03;
3; Mismatches 0; Indels 0;
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Vandesprace, A.E., Sorrells, W.E., Park, W.D., Ayres, N.M.,
Vandesprace, S.W., Paul, E. and McCouch, S.R.
Anchor Probes for Comparative Mapping of Grass Genera
Theor. Appl. Genet. 97, 356-369 (1998)
Contact: McCouch SR
Dept Plant Breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 others
                  Contract: Sikela JM
Contract: Sikela JM
Department of Pharmacology
University of Colorado Health Sciences Center
Box C336, 4200 E. 9th Ave, Denver CO 80262-0236
Tel: 3032708637
Fax: 3032707097
Email: nikki@tally.uchsc.edu
Seq primer: M13 Reverse.
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/cultivar="IR36"
/db_xref="RiceGenes:RZ612"
                                                                                                                                                                                                                                          /organism="Mus musculus"
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  Unpublished (1995)
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Best Local Similarity 80.0
Matches 12; Conservative
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetracdon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetracdon.
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0
                                                                 clone
                                                                                                                                                                      GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 216)
Beler, D. and Brady, K.
Mouse brain cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                      Tetraodontidae; Tetraodon.
1 (bases 1 to 215)
0 (boses-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 215)
Roest-Crollius, H. Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Welssenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                         Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon higroviridis
                                          CNS032CC 215 bp DNA GSS 15-MAY-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clo 206N11 of library G from Tetraodon nigroviridis, genomic survey
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Stratagene Mus musculus CDNA 5'end, mRNA
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Pred. No. 2.3e+03;
); Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 others
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/db_xref="taxon:99883"
/clone="206N11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="G"
/note="Genoscope sequence ID
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ALZ24661.1 GI:7883532
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80.0%;
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R74725.1 GI:849928
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80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
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54 GCTCCACTTGCTCCA 40
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/clone_lib="Owar; 2 (OV2)"
/clone_lib="Owar; 2 (OV2)"
/note="Organ: Mix of ovaries of varying immature stages
/note="Organ: Mix of ovaries of varying immature stages
/note="Organ: Mix of ovaries of varying immature stages
/note="Organ: Mix of ovaries of ovaries of rom Lambda
Zap II; Site_l: XhoI; Site_2: ECORI; The library was made
from poly-A RNA in the cloning vector lambda ZAP II.
clones to be sequenced were prepared by mass excision."
a 27 c 33 g 46 t
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RPCI-11-366P19.TV RPCI-11 Homo sapiens genomic clone RPCI-11-366P19
AQ554938
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/ssx="Male"
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/note="Vector: pBAce3.6; Site_1: EcoRI; Site_2: EcoRI;
### A 3 C 64 g 35 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.
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1 (bases 1 to 186)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
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                                                                                                                                                                                                                                                                                                                                         Score 13.8; DB 174; Length 154;
Pred. No. 2.2e+03;
3; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Lectaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
High quality sequence start: 9
High quality sequence stop: 125
                                                            Location/Qualifiers
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Best Local Similarity 80.0
Matches 12; Conservative
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CMO-HTO548-210 200-233-e07453=2000-02-21&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 2
High quality sequence start: 2
High quality sequence stop: 192.
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., Bordin,S., Costa,F.F., de Silvay,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Breskukma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
Site_7: To moreoff to the product of the profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Waterston,R. TITLE The WashI-HHMI Mouse E	JOURNAL Unpublished (1996) COMMENT COntact: Marra M/Mouse WashU-HHMI Mouse EST P	Washington University 4444 Porest Park Parku rel: 314 286 1800	Fax: 314 286 1810 Fmail: monseast@watson	TMAGE CONSORTIUM (info	MGI 283944 MGI 283944 - 28M13 rou	High quality sequence FEATURES Location/Oual	ř	/db_xref="tax /clone="IMAGE	/clone_lib="s /dev_stage="1	/lab_host="DH /note="Vector	polylinker; S	TGTTACCAATCTG double-strand	adapters (Pha			BASE COUNT 36 a 37 c ORIGIN		atch cal Similarity 80.0%;	Matches 12;	Qy 1 RCTCCAYTTRCTCCA 15	Db 134 ACTCCACTTGCTCCA 120	RESULT 2	BG159502/c LOCUS BG159502 154 bp DEFINITION OV2_5_B09.b1_A002 Ovar	seguence. N BG159502 BG159502.1 GI:126	KEYWORDS EST. SOURCE sorghum. ORGANISM Sorghum bicolor		REFERENCE 1 (bases 1 to 154)	o c	JOURNAL Unpublished (2000) COMMENT CONTACT: Cordonnier-Pr		Tel: 706 542 1860 Fax: 706 542 1805 Email: mmprattleuga.edu Seq primer: JEN REV
	Description	AA038484 mi83c09.r BG159502 OV2 5 B09	AQ554938 RPCI-II-3 RE171588 CM0-HT054	AL22461 Tetradon R7475 MDR0891R MO	AA231776 RZ612.F C	AI119961 uc23c06.r BB420958 BB420958	BB585089 BB585089 B75501 RPCII1-16K9	B40700 HS-1052-A1- M89352 CEL21F10 Ch	BF936011 IL2-NT019 BE650167 UI-M-BH3-	W34848 mc62a03.rl BF814907 IL5-CI014	A2238189 RPCI-23-7 AV185887 AV185887	AV192824 AV192824 AV194451 AV194451	AV196133 AV196133 C39835 C39835 Yuji	C42161 C42161 Yuji C42410 C42410 Yuji	C43142 C43142 Yuji C44203 C44203 Yuji	C47461 C47461 Yuji C48718 C48718 Xuji	D6/866 CELKU8/H/F AU110033 AU110033	AI215425 qhllblo.x C40410 C40410 Yuji	A1205294 qr25f08.x AV187143 AV187143	C43783 C43783 Yuji R38943 yd06f12.sl	R38942 yd06f111.s1 AV187242 AV187242	AV193885 AV193885 C47641 C47641 Yuji	C48090 AV193: RICS48:			EST	a muscutus cone ctone			Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.	. Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Steptoe, M., Tan, F., Underwood, K., Moore, B., B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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m="Mus musculus"
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t="bl108 (amptoilin resistant)"
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tranded cDNA was size selected, ligated to Eco RI (Pharmacia), digested with Not I and cloned into I and Eco RI sites of a modified pT7T3 vector I and Eco RI sites of a modified pT7T3 vector alion to a Cot = 5. Library constructed by Bentc allon to a Cot = 5. Library constructed by Bentc ond M.Fatima Bonaldo. RNA was kindly provided by crue XS 59
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fo@image.llnl.gov) for further information.
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em\_estro16:\*
em\_estro17:\*
em\_estro18:\*